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                                                                                    March 1, 2004, 17:21:01; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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A;Cross-references: EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PID:9514256
C;Comment: This protein mediates the agglutination of erythrocytes with antibody and comp
C;Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine
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R; Kawasaki, N.; Itoh, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 198, 597-604, 1994
A; Title: Gene organization and 5' flanking region sequence of conglutinin: A C-type mamme A; Reference number: JC2396; MUID:94128104; PMID:8297370
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A; Molecule type: mRNA
A; Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R; Lu, J; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
B; Cochem. J. 292, 157-162, 1993
A; Title: The CDNA cloning of conglutinin and identification of liver as a primary site (A; Reference number: S33235; MUID: 93277452; PMID: 7684896
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Biol. Chem. 266, 2715-2723, 1991
A;Title: Primary structure of boxine conglutinin, a member of the C-type animal lectin A;Reference number: A23740; MUID:91131556; PMID:1993651
A;Accession: A23740
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A;Contents: annotation
R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sast. J. Immunol. 153, 173-180, 1994
A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship A;Reference number: 146010; MUID:94267222; PMID:8207234
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A;Residues: 21-54;75-86, X', 88-89, X', 91, X', 93-94;208-209, X', 211-227 «KAW>
A;Residues: 21-54;75-86, X', 88-89, X', 91, X', 93-94;208-209, X', 211-227 «KAW>
A;Reperimental source: secum
R;Lu, J; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Bur. J. Biochem. 215, 793-799, 1993
A;Title: Structural similarity between lung surfactant protein D and conglutinin. A;Reference number: S35044; MUID: 93358905; PMID: 8354286
A;Accession: S35044
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A; Molecule type: protein
A; Mostandes 75-86, X', 88-89, X', 91,'I' < LUA>
A; Mostandes 15-86, X', 88-80, X', 91,'I' < LUA>
R; Young, N.M.; Leon, M.A.
R; Young, N.M.; Leon, M.A.
B; Oomann. 143, 645-651, 1987
A; Title: The carbohydrate specificity of conglutinin and its homology to proteins
A; Reference number: A29416; MUID:87184551; PMID:3566740
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A;Contents: annotation
B;Contents: A.C.; Sim, R.B.
R;Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 293, 15-19, 1993
Biochem. J. 293, 15-19, 1993
A;Title: Research Communication. Localization of the receptor-binding site in the A;Title: Research Communication. Localization of the receptor-binding site in the A;Title: Research Communication. Localization of the receptor-binding site in the A;Title: Research Communication.
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A; Residues: 1.17.7, H',174-217,'A',219-271,'V',273-371 <LUU>
A; Cross.references: EMB1:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
A; Experimental source: live:
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R;Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N. Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A,Title: Cloning and sequencing of a cDNA coding for bovine conglutinin. A,Reference number: JN0450, MUID:93213261; PMID:8460993
A,Resession: MO450
A,Residente type: mRNA
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A,Residues: 21-209, 'S', 211-371 <LEE>
R,Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Blochem. Blophys. 305, 533-540, 1993
A,Tille: Differentiation of conglutination activity and A,Reference number: S36879; MUID:93384312; PMID:8373191
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A;Molecule type: DNA
A;Residues: 1-371 <LIO>
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Cispecies: Bos primigenius taurus (cattle)
Cipate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
CiAccession: 833603
Rilim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A;Tile: Structural similarity between bovine conglutinin and bovine lung surfactant pro
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: H84314
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.D.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483; PMID:11016950
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JN0450
conglutinin precursor - bovine
conglutinin precursor - bovine
N;Alternate names: C3D-binding protein
N;Contains: conglutinin-N
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JN0450; JC2396; $33235; A23740; S36879; S35644; I46010; A29416; S34054
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A;Rross-references: GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB:GN00138
C;Genetics:
A;Gene: ccp
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C,Superfamily: pulmonary surfactant protein D; C-type lectin homology
:F;248-367/Domain: C-type lectin homology <LCH>
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Pred. No. 31;
3; Mismatches
                                         Score 36; DB Pred. No. 6.5; 2; Mismatches
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A; Accession: H84314
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-277 <STO>
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                                         Query Match
Best Local S:
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upporture train process. Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
A;Rose, D.J; Mau, B.; Shao, Y.
Science 27, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: G65039
A;Accession: G65039
A;Accession: Title: Aibary
A;Seatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: 1-196 - CBLAT>
A;Accession: 1-196 - CBLAT>
A;Cross-references: GB.RE000347; GB:U00096; NID:g2367142; PIDN:AAC75661.1; PID:g1788965;
A;Experimental source: strain K-12, substrain MG1655
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-4ul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70890
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                      Cition transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum Calion transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum CiSpecies: Clostridium acetobutylicum CiSpecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 CiAccession: D97163, A: Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R; Nolling, J.; Bernett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Scatus: preliminary
A; Molecule type: DNA
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A;Cross-references: GB:AE001437; PIDN:AAK80095.1; PID:g15025128; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum AICC824
C;Genetics:
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Pred. No. 97;
1; Mismatches 0; Indels
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    Indels
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    1; Mismatches
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Best Local Similarity 87.5-
             7; Conservative
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C;Species: Bos primigenius taurus (cattle)
C;Accession: 145878
R;iiou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, R;iiou, L.S.; Castry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, R;iiou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, A.J.itle: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization q.A;Reterence number: 145878
A;Accession: 145878
A;A
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R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C; Quail, M.; Rutherford, M.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
C; Keywords: calcium binding; glycoprotein; hydroxylysine; hydroxyproline
F; 1-20/Domáin: signal sequence #status predicted <SiG>F; 1-20/Domáin: signal sequence #status predicted <MAT>
F; 21-371/Product: conglutinin #status predicted <MAT>
F; 46-214/Region: collagen-like
F; 55-371/Product: conglutinin-N #status predicted <MAZ>
F; 53-371/Product: conglutinin-N #status predicted <MAZ>
F; 54-8-369/Domain: C-type lectin homology <2.CH>
F; 54-8-369/Domain: C-type lectin homology <2.CH>
F; 63, 87, 99, 135, 141, 159, 162, 198, 210/Modified site: 5-hydroxylysine (Lys) #status experime
F; 78, 96, 108, 111, 129, 132, 147, 153, 171, 195/Modified site: 4-hydroxyproline (Pro) #status experimental
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Pred. No. 42;
1; Mismatches 1; Indels
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85.0%; Score 34; DB 2; Length 371;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels
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A,Molecule type: DNA
A,Residues: 1-754 <PAR>
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            77.8%; Pred. No. 71; ive 1; Mismatches
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: E70890
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-282 <COL>
A; Cross-references: GB:AL022073; GB:AL123456; NID:93256024; PIDN:CAA17851.1; FID:e125651
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Genetics
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Cybecie Ol-feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
CyAccession: AB3334
Rybelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2020
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB3334
daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain
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A,Residues: 1-370 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51837.1; PID:g17982584; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMIL0656
A;Map position: I
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Pred. No. 50;
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C;Superfamily: hypothetical protein H10107
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G3103
A;Atus: preliminary
A;Molecule: preliminary
A;Molecule: 1-426 <5TTO>
A;Cross references: GB:AE004850; GB:AE004091; NID:g9950560; PIDN:AAG07726.1; GSPDB:GN001: A;Genetics: A;Gen
                                                                                     CiSpecies: Pseudomonas aeruginosa
CiDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: C33103
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
Ristover, C.X.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
I. Lory, S.; Olson, M.V.
hypothetical protein PA4338 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Ayochetical protein orf470 [imported] - Guillardia theta nucleomorph
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Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 3; Mismatches 0; Indels
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Search completed: March 1, 2004, 17:36:28 Job time: 12.3333 secs

homo sapien mus musculu homo sapien mus musculu homo sapien

P49446 P23469 Q9d666 Q9y5i4 P97798 Q96jq0

sapien mus musculu homo sapien sus scrofa pseudomonas

sus scrofa bos taurus

P43030 P26994 P26891

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[5]
CHARCTERIZATION.
CHARCTERIZATION.
SKYLT A., Stroemqvist M., Egelrud T.;
Skytt A., Stroemqvist M., Egelrud T.;
Skytt A., Stroemqvist M. Egelrud T.;
Primary substrate specificity of recombinant human stratum corneum chymotryptic enzyme."
Chymotryptic enzyme."
Diochem. Biophye. Res. Commun. 211:586-589(1995).
-!- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE
                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin;
BEDILINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein
Egelrud T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Keratinocytes;

Yousef G.M., Scorilas A., Diamandis E.P.;
Mnolecular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3] SEQUENCE FROM N.A.
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal Overexpression of Erratum corneum chymotryptic enzyme mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning" expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                  253 AA.
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                                                                                                                                                                     ALIGNMENTS
APP1 HUMAN
PTPE MOUSE
PTPE HUMAN
U84A MOUSE
CHC2 HUMAN
NEO1 MOUSE
PCD16 HUMAN
SZO7 PIG
                                                                                                SZ07 PIG
EXSB PSEAE
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077755 trichosurus
P35246 bos taurus
Q8mhz9 bos taurus
P23805 bos taurus
P37908 escherichia
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                                                                                        March 1, 2004, 17:17:25; Search time 6 Seconds (without alignments) 78:105 Million cell updates/sec
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P37908 e
O60813 L
Q03157 n
P20433 F
P19999 z
P33706 c
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-
|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation
of precursors to inflammatory cytokines.
TISSUE SPECIFICITY: Abundantly expressed in the skin and is
expressed by keratinocytes in the epidermis. Very low levels are
also seen in the brain and kidney.
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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N'-LINKED (GLCNAC. . .) (POTENTIAL).
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PRINTS, PR00722; CHYMOTRYPSIN,
BMRAT; SM00200; TTYP, SPC; 1.
PROSITE; PS50240; TRYPSIN, DOM, 1.
PROSITE; PS00134; TRYPSIN, DOM, 1.
PROSITE; PS00135; TRYPSIN, SER; 1.
Hydrolase; Serine profease; Zymogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604438; -
GO: 60:0008236; F:serine-type peptidase activity; TAS.
GO: GO:0008544; Pepidermal differentiation; TAS.
InterPro; IPR009003; Cys. Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                            EMBL, L33404, AAC37551.1, -.
EMBL, AF166330, AAD49718.1; -.
EMBL, AF243527, AAG33360.1; -.
EMBL, AF332583, AAK69624.1; -.
PIR, A53968, A53968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27525 MW;
                                                                                                                                                                                                                                                                                                                                                                                   MERCPS; S01.300; -. Genew; HGNC:6368; KLK7.
MIM; 604438; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
PROPEP
CHAIN
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FK11 MOUSE STANDARD; PRT; 201 AA.

Q9DINT; Q9CERE4;
28-FEB-2003 [Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
FK506 binding protein 11 precursor (RC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPlase) (Rotamase) (19 kDa FK506-binding protein) 0; Gaps Local Similarity 100.1 les 9; Conservative 5 LLLPLOILL 13 1 LLLPLQILL 9 FK11 MOUSE 1D FK11 M 1D FK11 M 1D 28-FEB 1D 28-FEB 1D 28-FEB 1D 28-FEB 1D 18-FEB Matches RESULT 2 ò

Mus musculus (Mouse)

FKBP11.

```
(omega=0).

-!-SIMILARITY: Belongs to the FKBP-type PPIase family.

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                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEALING-SEGG; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa T., Fukunishi Y., Komon H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Arawa K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackehbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackehbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackehbush J.,

Ruchl P., Lowis S., Matsuo Y., Nikaido I., Pesole G., Ouackehbush J.,

Rakai K., Okido T., Stuuni M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Chons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayasahizaki Y.,

Functional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATESTED FROM THE STATE STATESTER FROM THE STATEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK003331; BAB22719.1; -.
EMBL; AK019132; BAB31559.1; -.
EMBL; BC037596; AAH37596.1; -.
HSSP; PC071; IFKJ.
MGD; MGI:1913370; FKbpl1.
Interpro; IPR01179; FKBP_PPIASE.
PFAM; PF00254; FKRP; 1.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10090;
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SEQUENCE
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PSPD_BOVIN
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEPURE-99027340; Pubmed=9801457;

A MEDLINE-99027340; Pubmed=9801457;

A Greenwood P.J., MCNatty K.;

A Greenwood P.J., MCNatty K.;

The inhibin alpha subunit of Australian brushtail possum (Trichosurus The inhibin alpha subunit of Australian brushtail possum (Trichosurus The inhibin alpha subunit of Australian brushtail possum (Trichosurus The inhibin alpha subunit of Australian brushtail possum (Trichosurus The inhibin alpha subunit of Australian brushtail possum (Trichosurus The Inhibin alpha SECRETION of POLLITROPIN ST THE PITUITARY GLAND.

I J. MOL. Endocrinol. 21:141-152(1998)

I J. MOL. Endocrinol. 21:141-152(1998)

I SERSECTIVENT, THE SECRETION OF POLLITROPIN ST THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GERM CELL ENVIOLEMENT AND MATURATION, ERRYTHROID DIFFERENTIATION, INSULIN SECRETION, NEAVE CELL SURVIVAL, ENRYCONIC AXIAL DEVELOPMENT, DEPRENDING ON THEIR SURVIVAL.

SUBBRYONIC COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontía; Phalangeridae; Trichosurus.
                                                              POTENTIAL.

FKS06 BINDING PROTEIN 11.

PPIASE, FKBP-TYPE.

S -> F (IN REF. 1; BAB31559).

S -> R (IN REF. 1; BAB31559).

W, 94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
                                                                                                                                                                                                                    Match 95.0%; Score 38; DB 1; Length 201; Local Similarity 88.9%; Pred. No. 1.9; es 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin alpha chain precursor.
PROSITE; PS00454; FKBP PPIASE 2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
Isomerase; Rotamase; Signal.
                                                                                    28 201 FK
57 144 PP
53 143 S
198 S
201 AA; 22137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHA TRIVU
077755;
                                                                                                            DOMAIN
                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                           Query Match
                                                                 SIGNAL
                                                                                         CHAIN
                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3

IHH TRIVU

IHH TRIVU

DT 15-JU

DT 1
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GO; GO:0008151; P:cell growth and/or maintenance; ISS.

GO; GO:007166; P:cell surface receptor linked signal transdu. .; ISS.

BR GO; GO:003028; P:cell-cell signaling; ISS.

BR GO; GO:003028; P:cell-cell signaling; ISS.

BR GO; GO:004554; P:hemcalcoin biosynthesis; ISS.

BR GO; GO:004554; P:hemcalcoin biosynthesis; ISS.

BR GO; GO:0045578; P:negative requiation of B-cell differentiation; ISS.

BR GO; GO:004558; P:negative requiation of cell cycle; ISS.

BR GO; GO:004508; P:negative requiation of follicle-stimulating. .; ISS.

BR GO; GO:004507; P:negative requiation of follicle-stimulating. .; ISS.

BR GO; GO:004507; P:negative requiation of follicle-stimulating. .; ISS.

BR GO; GO:004326; P:negative requiation of follicle-stimulating. .; ISS.

BR GO; GO:004339; P:neurogenesis; ISS.

BR GO; GO:004339; P:neurogenesis; ISS.

BR GO; GO:004399; P:neurogenesis; ISS.

BR FRINTS; PRO0699; INMIDIA.

BR FRINTS; PRO0699; INMIDIA.

BR REINTS; PRO0699; INMIDIA.

BR PRODER; PSOO199; TGF BETA. 1.

BR REINTS; PRO0699; INMIDIA.

BR PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; SMOO204; TGFB; I.

BR SMRRI; PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; PROPEP

BR SMRRI; PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; PROPEP

BR SMRRI; PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; PROPEP

BR SMRRI; PRODER; PSOO260; TGF BETA. 1.

BR SMRRI; PROPEP

BR SMRRIARIY.

BR SMRRI; PROPEP

BR SMRRIARIY.

BR SMRRIARIY.

BR SMRRI; PROPEP

BR SMRRIARIY.

BR S
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-!- FUNCTION: Contributes to the lung's defense against inhaled microorganisms. Binds strongly maltose residues and to a lesser exten other alpha-glucosyl moieties. It could participate in the extracellular reorganization or turnover of pulmonary surfactant.
-!- SUBSUNIT: Oligomeric complex of 4 set of homotrimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-7UL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (FSP-D).
SFTPD OR SFTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora; Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Lung,
MEDLINE-93170856; PubMed-8436402,
Lim B.L., Lu J., Reid K.B.M.;
"Structural similarity between bovine conglutinin and bovine lung surfactant protein. D and demonstration of liver as a site of synthesis of conglutinin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 323 BY SIMILARITY.
289 359 BY SIMILARITY.
323 320 INTERCHAIN (BY SIMILARITY)
48 48 N'LINKED (GLCNAC. .) (PO
144 144 N'LINKED (GLCNAC. .) (PO
266 266 N'LINKED (GLCNAC. .) (PO
361 AA, 38945 MW, D661CDF93CDAAB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 208-247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPD BOVIN STANDARD;
P35246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LLLPLOLLL 12
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us-09-905-083-33.rgp

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CONG BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
-!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfactant-associated protein: 2 collagenous, carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P35247; 1B08.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF001391; Collagen; 2.
Pfam; PF00059; lectrin c; 1.
PROSITE; P800619; CIPPE_LECTIN_1; 1.
PROSITE; P800619; CIPPE_LECTIN_1; 1.
PROSITE; P800619; CIPPE_LECTIN_2; 1.
PROSITE; P800619; CIPPE_LECTIN_2; 1.
PROSITE; P800619; CIPPE_LECTIN_2; 1.
SIGNAL; Lectin; Callagen; Repeat; Coiled coil.
SIGNAL; Lectin; Callagen; Repeat; Coiled coil.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M., Skjoedt K., Holmskov U.; "CL-6, a novel collectin highly expressed in the bovine thymus and liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN-LIKE.
COLLED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
B-YSHILARITY.
N-LINKED (GLCNAC. ) (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%; Score 34; DB 1; Length 369; 77.8%; Pred. No. 22; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collectin-46 precursor (CL-46) (46 kDa collectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X75911; CAA53510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 77.8
les 7, Conservative
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Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
"The CDNA Cloning of Conglutinin and identification of liver as a
primary site of Synthesis of conglutinin in members of the Bovidae.";
Biochem. J. 292:157-162(1993).
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R InterPro; IPR008160; Collagen.
R InterPro; IPR001804; Lectin_C.
R Pfam; PF01391; Collagen.
R Pfam; PF001891; Collagen.
R Pfam; PF001891; Collagen.
R PF01891; Collagen.
R PROSITE; PS00615; CIVPE LECTIN 1; 1.
R PROSITE; PS00615; CIVPE LECTIN 2; 1.
R PROSITE; PS00615; CIVPE LECTIN 2; 1.
R PROSITE; PS00615; CIVPE LECTIN 2; 1.
R Collagen; Repect; Calcium; Signal.
R SIGNAL
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93213261; PubMed=8460993; Suzuki Y., Yin Y., Makamiya N.; Makino M., Kurimura T., Wakamiya N.; "Cloning and sequencing of a cDNA coding for bovine conglutinin."; Biochem. Biophys. Res. Commun. 191:335-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POTENTIAL).
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COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                           elmidarity).
-!-SUBERLIOUAR LOCATION: Secreted.
-!- SUBERLIOUAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in thymus and liver.
-!- PTM: Hydroxylated (Potential).
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
SUBUNIT: Oligomeric complex of 4 set of homotrimers (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 34; DB 1; Length 371; 77.8%; Pred. No. 22;
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108AC45A91420E83 CRC64;
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01.NOV-1991 (Rel. 20, Created)
01.PEB-1994 (Rel. 28, Last sequence update)
01.-CT-1.996 (Rel. 34, Last annotation update)
Conglutinin precursor.
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-94215917; PubMed-8163202;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
Bovine conglutinin (BC) mRNA expressed in liver: cloning and
characterization of the BC cDNA reveals strong homology to surfactant
                                                                                                                                                                                                                                                                    MEDLINE=94128104; PubMed=8297370;
Kawasaki N., Itoh N., Kawasaki T.;
"Gene organization and 5'-flanking region sequence of conglutinin: a
C-type mammalian lectin containing a collagen-like domain.";
Biochem. Biophys. Res. Commun. 198:597-604(1994).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-371.
MEDLINE=91131556; PubMed=1993651;
Lee Y.-M., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.;
"Primary structure of bovine conglutinin, a member of the C-type animal lectin family.";
J. Biol. Chem. 266:2715-2723(1991).
                                                                                                                                                        MEDINE=94267222; PubMed=8207234;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
"Bovine conglutinin gene exon structure reveals its evolutionary
relationship to surfactant protein-D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14085; BAA03170.1; -.
EMBL; X71774; CAA5065.1; -.
EMBL; L18871, AAA50126.1; -.
EMBL; U06805, AAB60624.1; -.
EMBL; U06854; AAB60624.1; -.
EMBL; U06855; AAB60624.1; JOINED.
EMBL; U06856; AAB60624.1; JOINED.
EMBL; U06857; AAB60624.1; JOINED.
EMBL; U06857; AAB60624.1; JOINED.
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                                                                                                            Gene 141:277-281(1994).
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D25299;
D25300;
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STRAIN=K12 / MG1655;
MEDLINE=Y4246617; PubMed=9278503;
Blattner F.R., Punkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                     R PIR; /148678; 145878.

R PIR; /JM6450; JM6450.

R HSSP; P35247; JB08.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR008160; Collagen.

R InterPro; IPR001304; Lectin_c; 1.

R PF03191; Collagen; 3.

R ProDom; PD000007; Clg_Mbelx; 1.

R PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

R PROSITE; PS00015; C_TYPE_LECTIN_2; 1.

R PROSITE; PS00015; C_TYPE_LECTIN_2; 1.

R PROSITE; PS00019; C_TYPE_LECTIN_2; 1.
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CELL ATTACHMENT SITE (POTENTIAL).
R > H (IN REF. 2 AND 3).
K -> S (IN REF. 2 AND 3).
K -> S (IN REF. 2).
E -> V (IN REF. 2).
E -> V (IN REF. 2).
E -> V (IN REF. 2).
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Pred, No. 22;
1; Mismatches 1; Indels
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C-TYPE LECTIN (SHORT FORM).
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MEDLINE=97349980; PubMed=9205837;
EMBL; D25301; BAA04983.2; JOINED
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NCBI_TAXID=562;
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Local Similarity 77.8%;
hes 7; Conservative 1
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371 AA;
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                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.5%; Score 33; DB 1; Length 435; 87.5%; Pred. No. 40; ive 1; Mismatches 0; Indels
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submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the MAPE family.
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMIIARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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30-WAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypochhetical protein D/845024.2 (Fragment).
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypotherical protein DJ845024.5 (Fragment)
Homo sapiens (Human).
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Best Local Similarity 87.5
Matches 7; Conservative
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298 LVPLQILL 305
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NON_TER 435 43
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                                                                                                                                      NCBI_TaxID=9606;
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  Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C., Yamagata S., Horiuchi T.; Pasamoto R., Bequence of the Escherichia coli "Construction of a contiguous 874-kb sequence of the Escherichia coli analysis of its sequence features.";
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                                                                                                                                                                                                                                                                       STRAIN=B178;
MEDLINE=88319942; PubMed=1045760;
Liphinska B., Xing J., Ang D., Georgopoulos C.;
"Sequence analysis and transcriptional regulation of the Escherichia coli grpE gene, encoding a heat shock protein.";
Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 2 CBS domains.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 199 THAT PRODUCES TWO ORFS.
-!- CAUTION: Ref.3 sequence differs from that shown due to numerous frameshifts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rudd K.E.;
Unpublished observations (AUG-1994).
-!- SUNCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO
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REMBL; AECO0347; AAC75662.1; ALT FRAME.

REMBL; D90888; BAAC6497.1; ALT FRAME.

REMBL; NOORS ANNOTATED_CDS.

RECOGENE; BG12442; yfjD.

RICEPTO; IPR00550; CBS.

RICEPTO; IPR00551; CBS domain.

Rem; PF00571; CBS; 2.

Rem; PF00571; CBC; Lranspt-asc.

Rem; PF00571; CBC; Lranspt-asc.

Rem; PF00571; CBC; Lranspt-asc.

Rem; PF00571; CBC; Lranspt-asc.

Rem; PF00571; CBS; 1.

Rem; PF01595; DUF21; 1.

Repeat; Transmembrane;

Remit of Complete CBS; 1.
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ID YA06_HUMAN
AC O60813;
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MEDLINE=96139497; PubMed=8576160;
Beher D., Hesse L., Masters C.L., Multhaup G.;
Requisition of amyloid protein precursor (APP) binding to collagen and "Requistion of the binding sites on APP and collagen type I.";
J. Biol. Chem. 271:1613-1620(1996).
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Homayouni R., Rice D.S., Sheldon M., Curran T.;
"Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                       APPI MOUSE STANDARD; PRT; 653 AA.

Q03157; Q8VC38;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
APLP1.
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BDILINE=93066322; PubMed=1279693;
Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
Solomon F.;
                                                                  Query Match
Best Local Similarity 87.5%; Score 33; DB 1; Length 500;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 0; Indels
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500 500
500 AA, 58247 MW, 1895CD8A8F14B7C3 CRC64,
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Matches 7; Conservative
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Homo sapiens (Human)
   PIR; S25656; S25656.
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198 AA;
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ENDOCYTOSIS SIGNAL.
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01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/LEU-2).
                                                                                                                                                                            REQUIRED FOR COPPER(II) REDUCTION (BY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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N-LINKED (GLCNAC. .) (POTENTIAL).
Y-G. KEDUCED BINNING OF APBB1.
P -> PP (IN REF. 2).
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                                                          ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
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COLLAGEN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                          BASOLATERAL SORTING SIGNAL (BY
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Pred. No. 59;
1; Mismatches 1; Indels
 EXTRACELLULAR (POTENTIAL).
                             CYTOPLASMIC (POTENTIAL). COPPER-BINDING.
                                                                                                                                                                                            SIMILARITY)
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Pest Local 7; Conservative
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MEDLINE=86103103; PubMed=3936473;
Parres J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
Parres J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
Berricture of Leu-2/TB as deduced from the sequence of a cDNA clone.";
Behring Inst. Mitt. 77:48-55(1985).
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21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 42, Last amortation update)
T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/Leu-2).
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T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-85099337; PubMed=3871356;
Littman D.R., Thomas Y., Maddon P.J., Chess L., Axel R.;
"The isolation and sequence of the gene encoding T8: a molecule
defining functional classes of T lymphocytes.";
Cell 40:237-246(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%; Score 32; DB 1; Length 198; 77.8%; Pred. No. 30; 1; Mismatches 1; Indels
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
BY SIMILARITY.
F3EC093EADB05561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 A.A.
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MEDLINE=90035142; PubMed=2509342;
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Natabowns K. 1., Tokito S., Okumara K., Nakauchi H.;

Intransponentics 20139-39/1989).

National Control of expression of the gene encoding CDB alpha chain (Leumann CDB and C
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mannose-binding protein A precursor (MBP-A) (Mannan-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 18-42.
MEDLINE-87222358; PubMed=3584121;
MEDLINE-87222358; PubMed=3584121;
MEDLINE-8722358; Sannoh T., Kawasaki N., Kawasaki T., Yamashina I.;
"Serum lectin with known structure activates complement through the classical pathway.";
CELL SURFACE GLYCOPROTEIN CD8 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drickamer K., Dordal M.S., Reynolds L., Mannose-bhidhing proteins isolated from rat liver contain carbohydrate-recognition domains linked to collagenous tails. Complete primary structures and homology with pulmonary surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drickamer K., McCreary V.,
"Exon attucte of a mannose-binding protein gene reflects its
evolutionary relationship to the asialoglycoprotein receptor and
nonfibrillar collagens ";
J. Biol. Chem. 262:2582-2589(1987).
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                                                                                                        235 CYTOPLASMIC (POTENTIAL).
135 IG-LIKE V-TYPE.
115
27
36
45
59
93
88
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102
102
112
112
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1131
A; 25729 MW, FCCA29BAA73726BB CRC64;
                                                       EXTRACELLULAR (POTENTIAL).
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                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
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8 LLLPLALLL 16
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SEQUENCE
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ID MABA RAT
                                                       DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody.

-!-SUBUNT: Oligomeric complex of set of homotrimers.
-!-SUBUNT: Oligomeric complex of set of homotrimers.
-!-SUBCLIULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST PREDOMINANTLY IN THE WOUGH ENDOPLASMIC RETICCLUM AND IN THE GOLGI APPARATUS, AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES AND LISSOSNEES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL SPACE OF THE ORGANELLES, PROBABLY AS A LOCASLEY BOUND MEMBRANE PROTEIN.
-!-SIMILARITY: Contains I Collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-dependent manner. Is capable of host defense against pathogens, by activating the classical complement pathway independently of the
                                X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 124-238.
MEDLINE=92086855; PubMed=1721241;
Weis W.I., Kahn R., Fourme R., Drickamer K., Hendrickson W.A.;
"Structure of the calcium-dependent lectin domain from a rat mannose-binding protein determined by MAD phasing.";
Science 254:1608-1615(1991).
                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 124-238.
MEDLINE=93063338; PubMed=1436090;
Weis W. I., Drickamer K., Hendrickson W.A.;
"Structure of a C-type mannose-binding protein complexed with an oligosaccharide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99119227; PubMed=9922165;
Ng K.K.-S., Park-Snyder S., Weis W.I.;
"Ca2+-dependent structural changes in C-type mannose-binding
                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 84-238.
MEDLINE=95219384; PubMed=7704532;
Weis W.I., Drickamer K.;
"Trimeric structure of a C-type mannose-binding protein.";
Structure 2:1227-1240(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 90-238
J. Biol. Chem. 262:7451-7454(1987),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.";
Biochemistry 37:17965-17976(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M14105; AAA98781.1; -.
EMBL; M14104; AAA98781.1; JOINED.
                                                                                                                                                                                                                                                                            Nature 360:127-134(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-92.
31-OCT-93.
03-APR-96.
03-APR-96.
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2KMB;
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4KMB;
1YTT;
1BCH;
1BCU;
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LKWT;
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InterPro; IPR003160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01031, Collagen; 1.
SMART; SM00034; CLECT; 1.
PR0STTE; PS00615; C_TYPE_LECTIN_1; 1.
PR0STTE; PS0041; C_TYPE_LECTIN_2; 1.
Complement pathway; Membrane; Mannose-binding; Calcium; Repeat; Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCEL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 32; DB 1; Length 238; 77.8%; Pred. No. 36; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                    (SHORT FORM) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    HYDROXYLATION. HYDROXYLATION (POTENTIAL).
                                                                                                                                                                                                                        MANNOSE-BINDING PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25308 MW; 1A927482B8A8CB3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD8 alpha chain precursor.
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                                                                                                                                                                                                                                      COLLAGEN-LIKE.
C-TYPE LECTIN (
HYDROXYLATION (
                                                                                                                                                                                                                                                                                                      HYDROXYLATION.
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                                                                                                                                                                                                                                                                                        HYDROXYLATION
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STRAIN=Beagle; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
183
192
198
PDB; 1KMY; 05-JUL-02.
PDB; 1KMZ; 05-JUL-02.
PDB; 1KX0; 05-JUL-02.
PDB; 1KX1; 05-JUL-02.
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230
238 AA;
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CD8A_CANFA
ID _CD8A_CANFA
                                                                                                                                                                                                                                      DOMAIN
DOMAIN
MOD_RES
MOD_RES
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DISULFID
DISULFID
CONFLICT
HELIX
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us-09-905-083-33.rsp

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MEDLINE=91264818, PubMed=2049082;
                                                                                                        MEDLINE #91373329; PubMed = 1894611;
  MEDLINE=91302311; PubMed=2071582;
                                                                                                                                                                                                                                                                                                                                                 enzyme.";
Biochem. J. 276:567-568(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M69137; AAAS2021.1; --
BMBL; M64269; AAAS2020.1; --
BMBL; M69136; AAAS2019.1; --
EMBL; X59072; CAA41796.1; --
BMBL; S61344; AABS6828.1; --
PIR; A40967; KYHUCM.
PDB; IKLT; 13-JAN-99.
                                                                                                                                                                                    SEQUENCE OF 22-247 FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE OF 26-60 FROM N.A.
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         chymase at 1.9 A.
                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                               rrssum=Heart
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                                                                                                                                                                                                                                                                               GO, GO:004210, CT-cell receptor complex, ISS.
GO; GO:0015026; F:coreceptor activity, ISS.
GO; GO:0015026; F:coreceptor activity, ISS.
GO; GO:0042515; F:protein binding; ISS.
GO; GO:0006955; F:immune response; ISS.
GO; GO:000710; F:T-cell activation; ISS.
GO; GO:000710; P:T-cell activation; ISS.
InterPro; IPR00310; Ig-like.
        Gorman S.D., Frewin MR., Cobbold S.P., Waldmann H.;

Gorman S.D., Frewin MR., Cobbold S.P., Waldmann H.;

alpha antigens. "Frewin M.R., Cobbold S.P., Waldmann H.;

alpha antigens. "184-188 (1994).

Tissue Antigens 43:184-188 (1994).

-!- FUNDTION! Identifies cytotoxic/suppressor T-cells that interact with MHC class I bearing targets. CDB is thought to play a role in the process of T-cell mediated Killing. CDB alpha chains binds to class I MHC molecules alpha -3 domains.

-!- SUBUNIT: In general heterodimer of an alpha and a beta chain linked by two disulfide bonds. Can also form homodimers.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
1018579779A5CB7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%; Score 32; DB 1; Length 239; 77.8%; Pred. No. 36; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCT1 HUMAN STANDARD; PRT; 247 AA.
P23946; Q16018;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Chymase precureor (EC 3.4.21.39) (Mast cell protease I).
CMA1 OR CYM OR CYH.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY
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MEDLINE=94378217; PubMed=8091416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 119 B
156 156 N
239 AA; 26036 MW;
                                                                                                                                                                                                                                                                                       EMBL; L14287; AAB02294.1; -. HSSP; P01732; 1CD8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immune response; Signal.
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SMART; SM00406; IGv;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLLPLQILL 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Schediter N.M., Strobl S.,
J. Mol. 18101. 286:817-817(1999)

-!- FUNCTION: Major secreted protease of mast cells with suspected
roles in vasoactive poptide generation, extracellular matrix
degradation, and regulation of gland secretion.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Phe-|-xaa > Tyr-|-Xaa >
-!- SUBCELLULAR LOCATION: Mast cell granules.
-!- SUBCELLULAR: Desprise and placenta.
-!- SUBCELLULAR: Belongs to peptidase family $1. Granzyme subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=93265916; PubMed=8495723; Sukenaga Y., Kido H., Neki A., Enomoto M., Ishida K., Takagi K., Katunuma N.; "Purification and molecular cloning of chymase from human tonsils."; PERS Lett. 323:119-122(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99134936; Pubmed=9931257;
Pereira P.J.P., Wang Z.-M., Rubin H., Huber R., Bode W.,
Schechter N.M., Strobl S.;
Schechter N.M., Strobl S.;
The 2.2-A crystal structure of human chymase in complex with
succinyl-Ala-Ala-Pro-Phe-chloromethylketone: structural explanation
for its dipeptidyl carboxypeptidase specificity.";
J. Mol. Biol. 286:163-173(1999).
Caughey G.H., Zerweck E.H., Vanderslice P.;
"Structure, chromosomal assignment, and deduced amino acid sequence of a human gene for maet cell chymase.";
J. Biol. Chem. 266:12956-12963 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
WEDLINES-29062883, Pubmed-2400368;
MCGrath M.E., Mirzadegan T., Schmidt B.F.;
"Crystal structure of phenylmethanesulfonyl fluoride-treated human
                                                                                                                                                                                                                                                                                                                                            Urata H., Kinoshita A., Perez D.M., Misono K.S., Bumpus F.M., Graham R.M., Husain A.; "Cloning of the gene and CDNA for human heart chymase."; J. Biol. Chem. 266:11173-17179(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenne D.E., Tschopp J.;
"Angiotensin II-forming heart chymase is a mast-cell-specific
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DR DDB; 1PUP; 02-WAR-99.

REMONIAN (1892) 1PUP; 02-WAR-99.

REMONIAN (1892) 20: 00.001229; 19.4AF-03.

REMONIAN (1892) 20: 00.001224; PREMONIAN (1892) 20: 00.
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FT STRAND 228 232
FT HELLX 233 236
FT HELLX 237 247
SQ SEQUENCE 247 AA; 27325 MW; DC1464A049ED6B00 CRC64;

Query Match
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps

Qy 1 LLLPLQILL 9
Db 2 LLLPLLLL 10
Search completed: March 1, 2004, 17:29:56
Job time: 7 secs
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; 0

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Q8n5n9 homo sapien
Q8vca9 mus musculu
Q8r5d5 mus musculu
Q8r2d5 pyrococcus
Q9v2d5 pyrococcus
Q9v2d5 pyrococcus
Q9ln2d lumpy skin
Q9ln2d lumpy skin
Q9ln2d lumpy skin
Q9ln2d salmonalla
Q8xq2 salmonalla
Q8xq2 salmonalla
Q8xq2 salmonalla
Q8xq2 mus musculu
Q8xq2 salmonalla
Q9xxq2 salmonalla
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                                                                                                                                               March 1, 2004, 17:20:41 , Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_arches:*
2: Sp_bacteria:*
3: Sp_lungi:*
5: Sp_nammal:*
5: Sp_nammal:*
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Q8VCA9
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Q91T40
Q91MZ4
Q9HPI3
Q863A1
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Q8Z802
Q97H76
Q8BJK7
Q9X620
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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mycobacte	brucella brucella shigella	salmonell pseudomor	Q8x9c3 escherichia Q9sea5 guillardia	Q82h48 streptomyce Q8eiy2 shewanella	pyrocc white	Q8vb59 white spot Q8brv0 mus musculu	Q8f8q9 leptospira	Q8mzy6 mamestra br	Q8mzv6 spodoptera	Q13970 homo sapien	юто вар юто вар	aimiri sci helicobact	Q8x6d3 escherichia Q922g5 mus musculu Q8uie2 agrobacteri							Euteleostomi; ; Homo.				ıses.								,	.4;
053979	QBYHY9 QBFZX1 QB3K08	Q8XFY3 Q9HW63	Q8X9C3 Q9SEA5 Q26479	Q82H48 Q8EIY2	Q8U289 Q8VBB6	Q8VB59 Q8BRV0	Q8F8Q9	QBMZYG	QBMZV6 QBMZV6 QBMZ76	013970	Q96QR6	9THVTQ 9THVTQ	Q8x6D3 Q922G5 Q8UIE2	ALIGNMENTS		PRT; 253 AA.	Created) Last semience indate)	dast annotation		; Craniata; Vertebrata; ; Catarrhini; Hominidae				: EMBL/GenBank/DDBJ database PEPTIDASE FAMILY S1.	 in activity: IEA.	EA.	s and peptidolysis; IEA.	crypsin. se_S1	se_SlA.	Z	М; 1. S; 1.	6	; 2D68B6A41B22A668 CRC64;
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e e	ጠ en en m en en	e e e		1 E E	3 3 3 8 8 8	32 32	32	1 CH C	N 23 C	100	3 3	32	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		П.	NSN9	-OCT-2002	-OCT-2003	mo sapien	karyota; mmalia; E	BI_TaxiD	SEQUENCE FRO TISSUE=Skin:	trausberg R	Submitted (J :!- SIMILARI	MBL; BC0320	30; GO:00082	30; GO: 00065	nterPro; IP	nterPro; IP fam; PF0008	RINTS; PROD SMART; SMOOO	PROSITE; PS50240; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1.	ROSITE; PSO Iydrolase; P	SEQUENCE 2
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0; Gaps

Query Match
100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels

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PRELIMINARY;
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Best Local Similarity
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                                                                                                                 Clethrionomys.
NCBI_TaxID=56223;
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                                                                                                                                               Mus musculus (Mouse),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                       Query Match 95.0%; Score 38; DB 11; Length 73; Best Local Similarity 88.9%; Pred. No. 4.2; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                 TISSUE-Salivary gland;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -.
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BCO22900; AAH22900.1; --
MGD; MGI:1913370; FKbp11.
GG; GO:0006457; P.procein folding; IEA.
InterPro; IPR001179; FKBP_PIPase.
PROSITE; PS00453; FKBP; PPIASE 1; 1.
PROSITE; PS00594; FKBP_PIPASE 2; 1.
SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;
                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN cDNA 1110002023 gene.
FKEP11 OR 1110002023RK.
                                                                              73 A.A.
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Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98152303; PubMed=9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain 4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.5%; Score 37; DB 8; Length 208; Best Local Similarity 88.9%; Pred. No. 17; Matches 8; Conservative 1; Mismatches 0; Indels
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Submitted (UUL.1999) to the EMBL/GenBank/pDBJ databases
EMBL, AJ2484813; CAB49063.1; -.
BIR; H75201; H75201.
InterPro; IPR008537; DUF819.
Pfan, PF05684; DUF819, 1.
Hypochetical protein; Complete proteome.
SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PYRAB01390.
PYRAB01390 OR PAB0088.
Pyrococcus abyssi.
                                                                                                                                             Clethrionomys gapperi (Southern red-backed vole).
Mitochondrion.
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SEQUENCE FROM N.A.

WEDLINE=20504483; PubMed=11016950;

REDLINE=20504483; PubMed=11016950;

REDLINE=20504483; PubMed=11016950;

REDLINE=20504483; PubMed=11016950;

REDLINE=20504483; PubMed=11016950;

REDLINE=20504483; PubMed=11016950;

REDLINE=2050483; PubMed=11016950;

REDLINE=2050483; PubMed=20; Thorsson V., Sbrogna J.,

RASHARA H.D., Lasky S.R., Ballaga N.S., Thorsson N.J., Hough D.W.,

Redler K., Cruz R., Parson M.J., Mongevine C.M., Dala H.,

Redler K., Cruz R., Mangevine C.M., Dala H.,

Redler R., Lowe T.M., Liang P., Riley M., Hood L., Jung K.-H.,

Rednome sequence of Halobacterium species NRC-1.";

REMBL, AE005072; AAG19864.1; -.

REMBL, AE005072; AAG19864.1; -.

REMBL, REMSL, REMSL, PICKERNE, REMBL, REMSL, REMSL
                                                                                                                                                                                                                                                                                                                                                     STRAIN=Neethiing Warmbaths LW;

Kara D., Afonso C., Wallace D.B., Kutish G.F., Stipinovich C.,

Lu Z., Veede F.T., Taliard L.C.F., Zaak A., Viljoen G.J., Rock D.L.;

"Molecular characterization of the South African vaccine strain and
the field isolate of lumpy skin disease virus.";

Submitted (AdG-2001) to the EMBL/GenBank/DBJ databases.

-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

EMBL, AF205258 AAR64971.;

-InterPro; IPR001841; Znf_ring.

Pfam, PF00097; zf_cABAG4; 1.

Pfam, PF00097; zf_cABAG4; 1.

Metal-binding; Zinc; Z
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                                                                                                  STRAIN=Neethling 2490;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.0%; Score 34; DB 12; Length 162; Best Local Similarity 88.9%; Pred. No. 55; Matches 8; Conservative 0; Mismatches 1; Indels
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,

LW Z., Vrede F.T., Taljaard L.C.F., Zask A., Viljoen G.J., Rock D.L.;

"Molecular characterization of the South African vaccine strain and
the field isolate of lumpy skin disease virus ";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF336128; AAK43550.1;

EMBL, AF336128; AAK43550.1;
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MEDLINE=21329495; PubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zeak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
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Stipinovich C., Vreede F.T., Kara P.D., Wallace D.B., Nel L.H.,
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Pred. No. 55;
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     0; Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro, IPR001841, Znf_ring.
Pfam, PF00097; zf_C3HC4,1.
SPQUEDCHELGAI protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 162 AA; 18782 MW; SF914A4080F729EE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (LAP/PHD-finger protein).
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LSDV010 OR LD010.
Lumpy skin disease virus (LSDV)
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Matches
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"Bovine surfactant protein D: Genomic characterization, chromosomal localization and tissue distribution.";

"Bovine surfactant protein D: Genomic characterization, chromosomal coalization and tissue distribution.";

"Bowline MAR-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ548848; CAD69922.1;

R EMBL; AJ548849; CAD69922.1;

R EMBL; AJ548849; CAD69922.1;

R MILE AJ548849; CAD69922.1;

R InterPro; IPRO01304; Calagen.

R InterPro; IPRO01304; Calagen.

R Pfam; PRO0159; lectin.c;

R Pfam; PRO0159; Lectin.c;

R R SMART; SMO034; CLETY;

R R SMART; SMO034; CLETY;

R PROSITE; PS50041; CTYPE_LECTIN.2;

R PROSITE; PS50041; CTYPE_LECTIN.2;

R PROSITE; PS50041; CTYPE_LECTIN.2;
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STRAIN=LIP2 / SGSC1412 / ATCC 700720;
MEDLINE=215448; Pubmed=11677609;
MEDLINE=215448; Pubmed=11677609;
MCCIelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                   Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.0%; Score 34; DB 6; Length 369; 77.8%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         surfactant protein D.
surfactant protein D.
4 474B7593508AESD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putative recombination protein.
                                                       01-JUN-2003 (TrEMBirel. 24, Created)
01-JUN-2003 (TrEMBirel. 24, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Surfactant protein D precursor:
                                    369 AA
                                                                                                                                                                                                                                                                                                                                                                                                               Potential
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                              1 20 PG
21 67 B1
245 369 B1
369 AA; 37405 MW;
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EMBL; AE008742; AAL19917.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCAI OR STM0983.
Salmonella typhimurium.
                                                                                                                                                         Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LLLPLSVLL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LLLPLOILL 9
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                 Q863A1
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         SSULT 9
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SEQUENCE FROM N.A.

STAIN—ANCE 634 / DSM 792 / VKOM B-1787;

WADLINE=21359125; PubMed=11466286;

A Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

A Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennet G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

RT "Genome sequence and comparative analysis of the solvent-producing

RT "Genome sequence and comparative analysis of the solvent-producing

RT "Genome sequence and comparative analysis of the solvent-producing

RT "Genome sequence and comparative analysis of the solvent-producing

RD BERLY ABOOT14; AAK80095.1;

DR GO: 00016020; C:membrane; IEA.

DR GO: 00016020; C:membrane; IEA.

DR GO: 00016022; F:ATPase activity; IEA.

DR GO: 00016022; F:ATPase activity; IEA.

DR GO: 00016022; F:Mydrolase activity; IEA.

DR GO: 00016022; F:Mydrolase activity; IEA.

DR GO: 00016022; F:Mydrolase BI-E2.

DR InterPro; IPR001404; Cation ATPase.

DR InterPro; IPR001609; H.ATPase.

DR InterPro; IPR00609; EI-E2 ATPase.

DR Fam; PF000699; Cation ATPase.

DR Fam; PF000699; Cation ATPase.

DR Fam; PF000690; Cation ATPase.

DR Pfam; PF000691; CATION ATPASE.

DR Pfam; PF000122; Hydrolase;

DR Pfam; PF00122; Hydrolase;

DR Pfam; Pf00122;
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                                                                                                                                                                                                                                                                                                                                   Clostridium acetobutylicum.
Barteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.0%; Score 34; DB 16; Length 845; Best Local Similarity 87.5%; Pred. No. 2.5e+02; Matches 7; Conservative 1; Mismatches 0; Indels
Best Local Similarity 77.8%; Fred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
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SEQUENCE 845 AA; 93779 MW; 401293AA1FF9D757 CRC64;
                                                                                                                                                                                                                                       01-0CT-2001 (TrEMBLrel 18, Created)
01-0CT-2001 (TrEMBLrel 18, Last sequence update)
01-0CT-2003 (TrEMBLrel 25, Last annotation update)
Cation transport P-type ATPase.
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01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
                                                                                                                                                                                                    PRT; 845 AA.
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PROSITE; PSO0154; ATPASE E1 E2; 1.
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                                                                                                                                                                                                    PRELIMINARY;
                                                                                                371 LLLPLOVAL 379
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                                                           1 LLLPLQILL 9
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QBBJK7
ID QBBJK
AC QBBJK
DT 01-MAI
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SEQUENCE FROM N.A.
STRATESPIL(64); ITSUE=Body;
STRATESPIL(64); ITSUE=Body;
The FANTOM CONSORTIUM,
The FANTOM CONSORTIUM,
The FANTOM COMMONE EXPORATION Research Group Phase I & II Team;
the RIKEN Genome Exportation Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
ENBL: AK083529; BA336942.1; -.
SEQUENCE 109 AA; 12276 MW; 852E75D4571F8DC6 CRC64;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
4030007E19R1K, protein.
4030007E19R1K, Mouse).
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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"Magnesium transport in Salmonella typhimurium: Sequence and
characterization of the corB, corC, and corD genes.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF130857; AAD31438.1;
InterPro. 1PR002550; CSS.
Pfam; PP01595; DUF21; 1.
SEQUENCE 196 AA; 21859 MW; B06659F7ESBAAIAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                puery Match 82.5%; Score 33; DB 11; Length 109; lest Local Similarity 66.7%; Pred. No. 60; Atches 6; Conservative 3; Mismatches 0; Indels
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01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINS-21085660; PubMed=1117651;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaaserland T., Gissi C., King B., Kochiwa H.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J.,

Schriml L.M., Staubli F., Szuuki R., Pesole G., Quackenbush J.,

Sakai K., Dokido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

B alake J., Boftell D., Bojunga N., Carninci M., Gariboldi M.,

Brownstein M.J., Bult C., Fleecher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fleecher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fleecher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fleecher C., Fujita M., Gariboldi M.,

Buctincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaetts P.,

A Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Toyo-oka K., Schoenbach C., Milttaker C., Wilming L.,

A Byrshizaki Y.,

Butti H., Toyo-oka K., Shopasha Y., Kawaji H., Kohtsuki S.,

R Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Butti A., Woologs; IMCT.

Butti A., Moologs; IMCT.

Butti A., Moologs; IMCT.

Butti A., Moologs; IMCT.

Butti A., Shoologs; Baballol;

Butti A., Shoologs;

Butti A., Shoologs;

Butti A., Shoologs;

Butti A., Shoologs;

Butti A., 
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SEQUENCE 196 AA; 17777 MW; 2136738FD496D815 CRC64;
NCBI_TaxID=10090;
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Search completed: March 1, 2004, 17:34:44 Job time: 32.3333 secs

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March 1, 2004, 17:21:46; Search time 11.8889 Seconds (without alignments) 39.081 Million cell updates/sec
GenCore version 5.1.6 Copyright %c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA.\*

1. /cgn2 6/pcdata/2/iaa/5A\_COMB.pep:\*
22. /cgn2 6/pcdata/2/iaa/5B\_COMB.pep:\*
3. /cgn2 6/pcdata/2/iaa/6A\_COMB.pep:\*
4. /cgn2 6/pcdata/2/iaa/6B\_COMB.pep:\*
5: /cgn2 6/pcdata/2/iaa/PcTUS\_COMB.pep:\*
6: /cgn2 6/pcdata/2/iaa/PcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	!			Appli				, Appl	Appli	App1:	Appli	Appli	App1i	Appli	Appli	Appli	Appli	-		O, Appl				, App	, App			, Appl
	r.	34	34	,	33	12	4,	2	4,	4,	N	m	7	ď	m	'n	ď	40	50	40	ທິ	44	'n.	75	75	75	75	75
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	QI	US-09-502-600-34	US-09-918-243-34	-41	-94	US-08-557-146-12	-09-027-33	US-09-154-344-12	-09-644-6	US-09-654-600A-4	-08-557-14	4-87	ű	8	US-09-210-084-3	US-09-764-762-3	-US96-04294-	19-502-600-	US-09-502-600-50	US-09-918-243-40	-09-918-243-5	US-08-944-483-44	5223425-8	US-08-485-455D-75	US-08-482-130C-75	7	US-08-906-769-75	US-08-906-616-75
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ORGANISM: Homo sapiens

LENGTH:

Sequence 75, Appl Sequence 17,	17,
US-08-817-795-75 US-08-485-4438-75 US-08-012-431-75 US-09-012-692-75 US-09-012-692-75 US-08-613-75 US-08-613-75 US-08-485-4458-17 US-08-484-13-01-17 US-08-817-795-17 US-08-817-795-17 US-08-817-795-17 US-08-817-795-17 US-08-817-795-17 US-08-817-795-17 US-08-817-795-17 US-08-906-769-17 US-08-906-769-17 US-08-906-769-17 US-08-906-769-17 US-08-906-769-17 US-08-906-769-17	1 1
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#### ALIGNMENTS

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RESULT 1
US-005-602-600-34
US-005-602-600-34
Sequence 34, Application US/09502600A
Patent No. 6294344
| GENERAL INFORMATION:
APPLICANT: 0'Brien, Timothy J.
ITILE OF INVENTION: Compositions and Methods for the Early Diagnosis of TILLE OF INVENTION: Compositions and Methods for the Early Diagnosis of FILE REFERENCE: D6223C1P-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: 09/039,211
| PRIOR PILING DATE: 03-14-1998
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Residues 58-66 of the SCCE protein US-09-502-600-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 34, Application US/09918243; Patent No. 6627403; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLVNERWVL 9
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APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TABLE-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: O'VER-XPICESSE In O'VARIAN CARCINOMA
TITLE REFERENCE: D6192
CURRENT APPLICATION NUMBER: U$/09/261,416A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Serine proteage catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 47; DB 3; Length 154; 100.0%; Pred. No. 0.29; tive 0; Mismatches 0; Indels
                                                                                 Query Match
100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                NAME/KEY: CHAIN
OTHER INFORMATION: Residues 58-66 of the SCCE protein
3-09-918-24-3-34
                                                                                                                                                                                                                                                   ESULT 3
78-09-261-416-7
78-09-261-416-7
Sequence 7, Application US/09261416A
Patent No. 6291663
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/08944483;
Patent No. 6232456;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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                                                                                                                                                                                    1 VLVNERWVL 9
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                                                                                                                                                              1 VLVNERWVL 9
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-944-483-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-261-416-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7
FEATURE:
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US-08-557-146-12
US-08-557-146-12
Sequence 12, Application US/08557146
Pacent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lennart
ITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
ITLE OF INVENTION: Brown (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 47; DB 3; Length 224; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: U.S.A.
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1103326-181
                                                                                                                                                                                                                            NAME: Becker, Cheryl L.
REGISTATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPHONE: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFRENCE/DOCKET NUMBER: 1103:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 225 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                            FILING DATE:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                     linear
           CLASSIFICATION:
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US-09-654-600A-4
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                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09027337B

Batent No. 5972616

GENERAL INFORMATION:

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: Breast and Ovarian Carcinomas

FILE REFERENCE: D6664

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 4.
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OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
OTHER INFORMATION: similar domain in TADG-15
                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE BADDRESS:
ADDRESSEE: White & Case, Patent Department
                                                                                          Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: White & Case, Patent Department
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 12, Application US/09154344
; Patent No. 5981256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VLVNERWYL 38
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown
                                                    -08-557-146-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 225
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JS-09-027-337-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08557146
Patent No. 5834200
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 47; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.49; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 47; DB 4; Length 225; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REPERNCE/DOCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids TYPE: amino acids TOPOLOGY: linear
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein
US-08-557-146-2
                                                                                                                                                                                                   OTHER INFORMATION: SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 VLVNERWYL 66
                                                                                                                                                                                                                                                                                                                                                                                               30 VLVNERWYL 38
                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLVNERWVL 9
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US-08-824-874-3
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IS-08-557-146-2
                                                                                          SEQ ID NO 4
LENGTH: 225
                                                                                                                                        TYPE: PRT
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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Patent No. 5981256

GENERAL INPORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 47; DB 2; Length 253; 100.0%; Pred. No. 0.49; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            CURPLY 353.4

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATION
SOFTWARE: Faited Herewith
FILING DATE: Filed Herewith
APPLICATION NUMBER:
FILING DATE: Filed Herewith
REGISTATION NUMBER:
FILING DATE: ATTORNATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REGISTATION NUMBER: 36,749
REGISTATION NUMBER: 36,749
RELEPHONE: 415-865-055
TELEPHONE: 415-865-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INPORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preet,
ITITLE OF INVENTION: NOVEL KALLIKREIN
ITITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0
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CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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100.0%; Score 47; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         DB 3; Length 253;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09210084
; Patent No. 6197511
; Patent No. 619751
; APPLICANT: Hillman, Jennifer L. APPLICANT: Lai, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
INDERSORE: SEQUENCES: STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 34304
COUNTRY: USA
ZIP: 34304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: FREESEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/824,874
FILING DATE:
THORD BATE:
THORD BATE:
THORD BATE:
FILING DATE:
FILI
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatch
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TYPE: amino acid
STRANDEDNESS: single
LENGTH: 253 amino acids
TYPE: amino acid
REALINDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLVNERWYL 66
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; CLONE: 532504
US-09-210-084-3
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US-09-764-762-3
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Patent No. 6093397
GENERAL INFORMATION: Eric P.
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
TITLE OF INVENTION: RELATED SEGUENCE:
TITLE OF INVENTION TO COMPATE SEGUENCE:
TITLE OF INVENTION TO S
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                             CURRENT APPLICATION DATA: PC-LOS/MS-LOS
SOFTWARE: PETENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: VS/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRICE APPLICATION:
PRICE APPLICATION:
PRICE APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: 35,372
REGISTRATION NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.49;
Lag 0; Indels
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100.0%; Score 47;
Best Local Similarity 100.0%; Pred. No. (
Matches 9; Conservative 0; Mismatche
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
ATTORNEY/AGENT 1NFORMATION:
NAME: Blalock, DOING K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 317-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
IENGTH: 253 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-154-344-2
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Query Match 100.0%; Score 47; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 0.49; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: DSA

ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:

MEDILUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASISED for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/210,084

FLING DATE: 16-Jan-2001

CLASSIFICATION NUMBER: 09/210,084

FLING DATE: MARRY: 16-Jan-2001

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36/749

REGISTRATION NUMBER: 36/749

RESTENDE/DOCKTT NUMBER: 36/749

RESTENDE/DOCKTT NUMBER: 36/749

TELEROWAUTION INFORMATION:

TELEROWAUTION INFORMATION:

TELEROWAL 15-845-166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LINGTH: 23 amino acids

STRANDEDISS: single

TYPE: amino acid

STRANDEDISS: single

TYPE: amino acid

STRANDEDISS: single

LIBRARY: Generank

LIBRARY: LIBRARY: LIBRARY: FIRERY: F
Sequence 3, Application US/09764762
Patent No. 6472155
GENERAL INPORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE S. 5
CORRESPONDENCE DADRESS:
STREET: 3174 Forter Plarmaceuticals, Inc.
STREET: 3174 Forter Daive
STATE: CA
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Search completed: March 1, 2004, 17:38:24 Job time : 12.8889 secs

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(without alignments) 55.820 Million cell updates/sec
                                                                                                                   March 1, 2004, 17:16:55; Search time 45.5556 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               1586107 segs, 282547505 residues
                                                                             protein - protein search, using sw model
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Listing first 45 summaries ost-processing: Minimum Match 0%
Maximum Match 100% Jatabase :

3: geneseg22000s:\* 4: geneseg2200ss:\* 5: geneseg2200ss:\* 6: geneseg2203ss:\* 7: geneseg2203ss:\* 8: geneseg2203ss:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aae08239 Human str	Ada05740 Human NOV	78	8 Human	Ada05736 Human NOV	Ada05744 Human NOV	2 Human	Ada05742 Human NOV	Ada05732 Human NOV	Ada05734 Human NOV	Aar67888 Human str	Aaw05383 Human amy	Abb84421 Human SCC	Human	Aau82740 Amino aci	Abu07440 Protein d	Abu07471 Protein d	Abr58471 Human str	Adb80484 Ovarian c	Aab21326 Human HSC	Aae08245 Human str	Aae08255 Human str	9 Bovine S	Abb84420 Porcine S	Aay28590 Human Fac
	AAE08239 Aa	ADA05740 Ad	ABG23378 Ab	ADA05738 Ad	ADA05736 Ad	ADA05744 Ad	7	ADA05742 Ad	ADA05732 Ad	4	AAR67888 Aa	AAW05383 Aa	ABB84421 Ab	ABB84406 Ab	AAU82740 Aa	ABU07440 Ab	ABU07471 Ab	ABR58471 Ab	4	AAB21326 Aa	AAE08245 Aa	AAE08255 Aa	ABB84419 Ab	ABB84420 Ab	AAY28590 Aa
DB ID			4 A													·	•				·		•		-
Length	თ	97	m	œ	σ	a	N	4	S	ហ	S	S	ŧŊ	S	S	ហ	253	ß	S	'n	σ	σ	4	249	$\vdash$
% Query Match	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	ä	91.5		85.1	83.0
Score	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47			47		43	40	40	39
Result No.	-	7	m	4	S	9	7	80	6		11						17								

Aae39994 Human adi	Aar05421 Human adi	Aae39992 Human adi	و		α	0,		14	Aaw10694 Human rec	Aaw12393 Mouse neu	Abb57219 Mouse isc	Aaw46773 Amino aci		Aaw41955 Flea seri	Abb60343 Drosophil	Adas0480 Human pro	Aaw41954 Flea seri	Aaw41953 Flea seri	Adb97555 Human MTS
AAE39994	AAR05421	AAE39992	AAW01196	AAB50593	ABG75788	AAW01165	AAB50561	AAW64261	AAW10694	AAW12393	ABBS7219	AAW46773	AAG79000	AAW41955	ABB60343	ADA50480	AAW41954	AAW41953	ADB97555
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228	250	253	64	64	81	223	224	232	260	260	260	233	233	237	243	247	258	258	271
83.0	83.0	83.0	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	6.08	78.7	78.7	78.7	78.7	78.7	78.7	78.7	78.7
39	39	33	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37
56	27	28	67	30	31	32	33	34	35	36	37	38	99	40	4.1	42	43	44	45

### ALIGNMENTS

RESULT 1

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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metaetsals, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                                                                    Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                          Human stratum corneum chymotrypsin enzyme peptide #3 (residues 58-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Page 103; 127pp; English.
           AAE08239 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                              07-FEB-2001; 2001WO-US003977.
                                                                                                                                                                                                                                                                                                                                               11-FEB-2000; 2000US-00502600.
                                                                             01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514676/56.
                                                                                                                                                                                                                                             WO200159158-A1.
                                                                                                                                                                                                                Homo sapiens.
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                                              AAE08239;
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AAE08239
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Sequence 9 AA;

Query Match

100.0%; Score 47; DB 4; Length 9;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

WPI; 2003-381626/36. N-PSDB; ADA05739.

Claim 1; Page 171; 586pp; English.

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                                                                                                                                                                                                                                                                                                                  immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabeter; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                      Gaps
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                                                                                                                                                                                                                                                                                                 human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Human NOV18e protein SEQ ID NO:100.
                                                                                                                                                                 ADA05740 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001; 20010S-0327417P

09-OCT-2001; 20010S-0328029P

09-OCT-2001; 20010S-0328044P

12-OCT-2001; 20010S-0328044P

15-OCT-2001; 20010S-033044P

17-OCT-2001; 20010S-033044P

17-OCT-2001; 20010S-033044P

17-OCT-2001; 20010S-0330409P

24-OCT-2001; 20010S-0330309P

24-OCT-2001; 20010S-0330266P

24-OCT-2001; 20010S-0333266P

19-APR-2002; 20010S-0333266P

19-APR-2002; 20020S-0373817P

19-APR-2002; 2002US-0373817P

16-MAY-2002; 2002US-0373817P

16-MAY-2002; 2002US-0373817P

16-MAY-2002; 2002US-0373817P

16-MAY-2002; 2002US-0373817P

16-MAY-2002; 2002US-03138164P

16-MAY-2002; 2002US-0313103P

16-MAY-2002; 2002US-0313103P

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-038103PP

16-MAY-2002; 2002US-0381383PP

25-UNN-2002; 2002US-0381383PP

25-UNN-2002; 2002US-0381383PP

25-UNN-2002; 2002US-0381383PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2002; 2002WO-US031373.
                                                                                                                                                                                                                                06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                  1 VLVNERWVL 9
                                                                               1 VLVNERWVL 9
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Shimkets RA,
Eisen AJ, Gal
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                   ADA05740;
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The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising; in one or more described above and a carrier; (2) a kit comprising; in one or more or more containers, the composition described above; (3) an isolated mucleic acid molecule described above; (3) a cell a vector comprising the uncleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically breamed to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above collaboration of a disease associated with altered levels of expression of the above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for a serior above; (10) a method for identifying a potential therapeutic agent for a perhology associated with the polypeptide; (11) a method of cor or preventing a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide described above polypeptide. Novy correctivity of the polypeptide described above polypeptide in a method for protective, antibacterial, virunide, immunomodulator, cytostatic, nocropic, neuroprotective antiparkinsonian and antilipaemic are are and and antilipaemic activity of the polypeptide above polypeptide of useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the mucleic acid sorders and various disorders such as diabetes or obesity, infections, cachexia, cachexia, cachexia, inmune disorders, haematopoicite disorders and various disorders when the polypeptide as human Novy from the pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 6; Length 97; 100.0%; Pred. No. 0.87; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #23369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG23378 standard; protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
Best Society 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG23378
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conservation antibodies of exchaint and expressed sequence tags for identifying expressed conservation antibodies against it, detecting or quantitating a cutivity of (II) or to treat disease states involving (II). (II) is useful in sering an encipt markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The protein expression or biological activity. The convolvence applications in involving abstrant protein expression or biological activity. The protein expression of materials to fautations in the principle for genetic disorders or ther traits to assess biodiversity and to produce other types of deta and products dependent on DNA and and to produce other types of deta and products dependent on DNA and anino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the print way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 47; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA05738 standard; protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV18d protein SEQ ID NO:98.
                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                            Drmanac RT, Liu C, Tang YT;
                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 VLVNERWYL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLVNERWVL 9
                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS87565.
                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA05738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
```

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## W20031029424-A2.

## W2003102942-A2.

## W2003102942-A2.

## W2003102942-A2.

## W2003102942-A2.

## W2003102942-A2.

## W200310294-A2.

## W2
```

2002US-0373826P.

```
the activity of the polypeptide described above; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. Now; sequences have antidabetic, anotorotic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaemic attivities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to obsity, infections, candexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various probes, in chromosome mapping, tissue typing, preventive medicine and parmacogenomics. The present sequence represents a human NoVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
              តិតិតិតិស្តីស្តីស្តីស្តីស្តីស្តីស្តីស្តីស្តី
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Sequence 181 AA;

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100.0%; Score 47; DB 6; Length 181;
100.0%; Fred. No. 1.7;
tive 0; Mismatches 0; Indels 0; Gaps
1 VLVNERWVL 9
                                               δ
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39 VLVNERWYL 47

ADA05736 standard; protein; 198 AA. 06-NOV-2003 (first entry)

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabeter; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

Human NOV18c protein SEQ ID NO:96.

Homo sapiens.

WO2003029424-A2.

02-OCT-2002; 2002WO-US031373

05-0CT-2001; 200108-0327435F 05-0CT-2001; 200108-03274435F 09-0CT-2001; 200108-0328044F 09-0CT-2001; 200108-0328044F 09-0CT-2001; 200108-0328044F 09-0CT-2001; 200108-0328046F 12-0CT-2001; 200108-0328144F 17-0CT-2001; 200108-0339149F 18-0CT-2001; 200108-031039F 24-0CT-2001; 200108-0341058F 24-0CT-2001; 200108-0341058F 24-0CT-2001; 200108-0341058F 24-0CT-2001; 200108-034957F 01-NOV-2001; 200108-0346557F 2002US-0373815P AND STATE OF THE S

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG; Shinkets RA, Rochenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
     19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0373804P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381656P.
29-MAY-2002; 2002US-0381651P.
25-MAY-2002; 2002US-0391335P.
01-0CT-2002; 2002US-0391335P.
                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                              WPI; 2003-381626/36.
                                                                                                                                                                                       N-PSDB; ADA05735.
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Claim 1; Page 170; 585pp; English.

pharmacogenomics.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOVY). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more described above, (3) an isolated nucleic acid described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically briesence or amount of the above polypeptide for described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically bresence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a described above; (10) methods for determining the presence of the polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for one in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of correcting or pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the polypeptide; (12) a method for modulating a sequences have antidiabetic, anorettic, and antilipaemic activities, and can be used an used to disease, immune disorders such a Munan disorders such a Allahamer, pathology associated with a plane and antilipaemic and disorders haematopoletic disorders

Sequence 198 AA;

present invention.

0; Gaps 100.0%; Score 47; DB 6; Length 198; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.0

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3 07:49:11 2004
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterron E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. Human NOV18g protein SEQ ID NO:104. ADA05744 standard; protein; 224 AA. 05-OCT-2001, 20010S-0327435P.
05-OCT-2001, 20010S-0327435P.
09-OCT-2001, 20010S-0327435P.
09-OCT-2001, 20010S-0328044P.
09-OCT-2001, 20010S-0328044P.
09-OCT-2001, 20010S-0328044P.
12-OCT-2001, 20010S-0328044P.
17-OCT-2001, 20010S-033904P.
18-OCT-2001, 20010S-0339109P.
24-OCT-2001, 20010S-0349105P.
24-OCT-2001, 20010S-0349105P.
24-OCT-2001, 20010S-0349105P.
19-APR-2001, 20010S-0349105P.
19-APR-2002, 20020S-0373817P.
19-APR-2002, 2002US-0373817P.
19-APR-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373814P.
17-MAY-2002, 2002US-03738164P.
17-MAY-2002, 2002US-03738164P. 02-OCT-2002; 2002WO-US031373 (first entry) (CURA-) CURAGEN CORP. WPI: 2003-381626/36. N-PSDB; ADA05743 WO2003029424-A2. 06-NOV-2003 3SULT 6 

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically breaming the polypeptide acid molecule described above; (5) a cell presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a disease associated with altered levels of expression or the polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (11) a method for identifying a potential therapeutic or included for above; (11) a method for acidilation or the polypeptide; (12) a method for modulating or the polypeptide; (12) and (14) a method for protectic, and (14) a method for producing the above polypeptide; NOVX mammal; and (14) a method for producing the above polypeptide; NoVX and antilipaemic activities, and can be used an experibation or experience have antidiabetic, anoctoric, antibaterial, virucide, and antilipaemic activities, and an unand disorders such a shappen or obesity, infections, cancer or prevent metabolic disorders such as diabetes or obesity, infections, cancer and antilipaemic activities, haematopoietic disorders and warious or proceeding a polypeptide is useful in manufacturing a medicane a preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Claim 1; Page 172; 586pp; English. present invention. pharmacogenomics. 

Sequence 224 AA;

ö 100.0%; Score 47; DB 6; Length 224; 100.0%; Pred. No. 2.2; tive 0; Mismatches 0; Indels 0; Gaps 

AAB98502 standard; protein; 225 AA.

AAB98502;

03-AUG-2001 (first entry)

Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain. FXBXBXBXBXBXGXBXBXGXB

Human, TADG-15, cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.

Homo sapiens.

WO200129056-A1.

26-APR-2001.

20-OCT-2000; 2000WO-US029095.

New NOVX polypeptides and nucleic acids, useful for diagnosing,

```
The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9.20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
                                                                                                                                                                                              Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                       Example 10; Fig 1; 130pp; English.
                                                                                                            Tanimoto H;
                                                                (UYAR-) UNIV ARKANSAS.
                                                                                                                                                      WPI; 2001-381031/40.
                                                                                                          O'brien TJ,
```

2.2; hes 0; Indels 0; Gaps 100.0%; Score 47; DB 4; Length 225; 100.0%; Pred. No. 2.2; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 ....has 9, Conservative 1 VLVNERWVL 9 ò

Seguence 225 AA;

30 VLVNERWYL 38 Вb

ADA05742 standard; protein; 247 AA. Human NOV18f protein SEQ ID NO:102. 06-NOV-2003 (first entry) ADA05742; 

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; Gyvostatic; nootropic; neuroprotective; autiparkinsonian; antilpaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer, disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

Homo sapiens.

WO2003029424-AZ. 10-APR-2003

2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 02-OCT-2002; 2002WO-US031373. 02-OCT-2001;

09-OCT-2001; 09-OCT-2001; 12-OCT-2001; 09-OCT-2001;

20010G-0328029P-20010G-0328044P-20010G-0328649P-20010G-0329414P-20010G-0330442P-20010G-0330309P-20010G-0330309P-20010G-0341058P-17-OCT-2001; 18-OCT-2001; 22-OCT-2001;

present invention.

24-OCT-2001, 2001UG-0343629P.
29-OCT-2001, 2001UG-0345629P.
01-NOV-2001, 2001UG-034583FP.
19-APR-2002, 2002UG-0373860P.
19-APR-2002, 2002UG-037387P.
19-APR-2002, 2002UG-037387P.
19-APR-2002, 2002UG-0373864P.
22-APR-2002, 2002UG-037897P.
16-MAY-2002, 2002UG-0381037P.
16-MAY-2002, 2002UG-0381042P.
17-MAY-2002, 2002UG-0381642P.
28-MAY-2002, 2002UG-0381642P.
26-UNN-2002, 2002UG-03818381P.
25-UNN-2002, 2002UG-03818381P.
26-UNN-2002, 2002UG-03818381P. 

# (CURA-) CURAGEN CORP.

thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; curajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; kets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; en AJ, Gangolli EA, Rieger DK, Spaderna SK; Patturajan M, Shimkets RA, Smithson G, Eisen AJ, Ji W,

WPI; 2003-381626/36. N-PSDB; ADA05741. New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 172; 586pp; English.

The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carribed above; (3) an isolated nucleic acid described above; (3) an isolated nucleic acid containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically briefs to the polypeptide acid molecule described above; (5) a call comprising the above vector; (6) an antibody that immunospecifically breached or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition or a pathology associated with the polypeptide; (12) a method of mammal; and (14) a method for producing the above polypeptide in a muchod for protectic, antibacterial, virucide, and antilipaemic activities, and can be used above polypeptide in a syndrome associated with a human disease. In polypeptide is useful in manufacturing a medicament for treating a pathology associated with a human disease. Contain and various of sorders such as diabetes or obesity, infections, cachexia, cancer, and molecule may be used to diasease. In process, in chromosome mapping, tissue typing, preventive medicine and process, in chromosome mapping, tissue typing, preventive medicine or processer; in the processer is neared to the processe

us-09-905-083-34.rag

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RESULT 10
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                                                                                                                                                                                                                              immunomodulator; cytostatic; noctropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Octr T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
                                          Gaps
                   100.0%; Score 47; DB 6; Length 247;
100.0%; Pred. No. 2.5;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                     human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                     ADA05732 standard; protein; 250 AA.
                                                                                                                                                                                                 Human NOV18a protein SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2001, 2001US-0327459F.
05-OCT-2001, 2001US-0327449F.
09-OCT-2001, 2001US-0327449F.
09-OCT-2001, 2001US-0328044F.
09-OCT-2001, 2001US-0328044F.
09-OCT-2001, 2001US-0328044F.
12-OCT-2001, 2001US-0328044F.
17-OCT-2001, 2001US-0339049F.
18-OCT-2001, 2001US-033904P.
24-OCT-2001, 2001US-03495P.
25-OCT-2001, 2001US-03495P.
25-OCT-2001, 2001US-03495P.
26-OCT-2001, 2001US-03495P.
27-OCT-2001, 2001US-03495P.
29-OCT-2001, 2001US-03495P.
29-OCT-2001, 2001US-03495P.
29-OCT-2001, 2001US-03495P.
29-OCT-2001, 2001US-03495P.
19-APR-2002, 2002US-0373815P.
19-APR-2002, 2002US-0373815P.
16-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0381038P.
16-MAY-2002, 2002US-0381038P.
17-MAY-2002, 2002US-0381042P.
17-MAY-2002, 2002US-0381642P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-2002; 2002US-0391335P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2002; 2002US-0383831P.
                                                                                                                                                                                                                                                                                                                                                          02-OCT-2002; 2002WO-US031373
                                                                                                                                                                            06-NOV-2003 (first entry)
        Query Match
Best Local Similarity 10v...
3; Conservative
                                                                              44 VLVNERWVL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                            1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                 WO2003029424-A2.
Sequence 247 AA;
                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                      10-APR-2003
                                                                                                                                                        ADA05732;
                                                                                                                        ESULT 9
                                                                               Ω
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The present invention describes NoVX proteins, where X can be 1 to 55 cd e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit composition or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell of comprising the nucleic acid molecule described above; (5) a cell of presence or amount of the above polypeptide fescribed above; (7) methods for determining the paragraph of identifying an agent that binds to the above of adsease associated with altered levels of expression of the above a disease associated with altered levels of expression of the above and pathology that is related to an aberrant expression of a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for aberrant physiological interactions of the polypeptide; (11) a method of secretarial physiology that is related to an aberrant expression or a pathology that is related to an aberrant expression or a pathology associated with the polypeptide; (12) a method for modulator of activity or of latency or predisposition to spending a pathology associated distributed described above; (13) a method of subjective described above polypeptide in a method for producing the above polypeptide in a method for producing the above polypeptide or the nucleic or proventing a pathology associated with the above polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disperser, hammed adabetes such as diabetes or obesity, infections, cardexia, cancer, d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenemics.
                              Berghs C, Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 47; DB 6; Length 250; 100.0%; Pred. No. 2.5; tive 0; Mismatches 0; Indels
                              Rothenberg ME, Leach MD, Agee ML, ngolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 169-170; 586pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA05734 Btandard; protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NOV18b protein SEQ ID NO:94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 9; Conservative
Shimkets RA, Rotuc...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 VLVNERWVL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLVNERWVL 9
                                                                                                                                         WPI; 2003-381626/36.
N-PSDB; ADA05731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA05734;
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neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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Homo sapiens.

WO2003029424-A2.

02-OCT-2002; 2002WO-US031373.

2001US-0327917F. 2001US-0328029P. 2001US-0328044F. 2001US-0328414F. 2001US-032414F. 2001US-032414F. 2001US-033410SF. 2001US-033410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF. 2001US-03410SF.

-APR-2002, 2002US-0373884P.
-APR-2002, 2002US-037497P.
-AAY-2002, 2002US-0381037P.
-MAY-2002, 2002US-0381038P.
-WAY-2002, 2002US-0381042P. 19-APR-2002;

2002US-0381642P. 2002US-0383656P. 2002US-0383831P. 01-OCT-2002; 2002US-00262511. 29-MAY-2002;

# (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Carterron E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG;
Shinkets RA, Rochamberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Shimkets RA, Eisen AJ, G

WPI; 2003-381626/36. N-PSDB; ADA05733 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 described above and a carrier; (1) a kit comprising, in one or more containers, the composition described above; (3) an isolated nuclear acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (3) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the breache or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the passance of a monut of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic

Disclosure; Page 97; 137pp; English.

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method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or preventing a pathology associated with the above polypeptide in a method for modulating or preventing a pathology associated with the above polypeptide. Now; sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The comparative of unautilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic actid modecute may be used to disapte or prevent metabolic disease, immune disorders such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's probes, in otheromosome mapping, tissue typing, preventive and present sequence represents a human NovX from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human stratum corneum chymotrophic recombinant enzyme (SCCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%; Score 47; DB 6; Length 252; Local Similarity 100.0%; Pred, No. 2.5; res 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR67888 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-IB000166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93DK-00000725.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 VLVNERWYL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYMB-) SYMBICOM AB.
                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1993;
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09-AUG-1995
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ABB84421 standard; peptide; 253 AA.

ABB8442:

ABB84421;

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Human amyloid precursor protein protease (AAW05181) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39781) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. B. coli) or eukaryotic (partic. AV-120 host cells. It is used to develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pssor. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
                                                                                                                                         100.0%; Score 47; DB 2; Length 253; 100.0%; Pred. No. 2.5; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 2; Length 253; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human amyloid precursor protein protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dixon EP, Johnstone EM, Little SP;
                                                                                                                                                                                                                                                                                                                       AAW05383 standard, protein, 253 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1996 (first entry)
                                                                                                                         (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                       58 VLVNERWYL 66
                                                                                                                                                                                                         1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT39783.
                                                                                                               Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9631122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                   AAW05383;
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, or grandly linked to a promoter that drives expression of heterologous soce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve to ramellorate a pathogenic condition, for development or resting of a cosmetic or a pharmaceutical formulation, and for the development of a cosmetic or a pharmaceutical formulation, and for the development of a cosmetic or a pharmaceutical formulation, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis. The mammal of the invention is also useful or the pidermal hyperkeratosis. The mammal of the invention is also useful compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal synonymous with human stratum corneum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the envention of the invention of the i
                                                                                                                                         SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protesse; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                               Human SCCE protein N-terminal fragment SEQ ID 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 37; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-2001; 2001CA-02332655.
                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2002; 2002WO-IBG01300.
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Best Local Similarity luc...

Best Local Similarity
                                            08-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Egelrud T, Hansson L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                         WO200262135-AZ.
                                                                                                                                                                                                                                                                            Homo sapiens.
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Gaps

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0; Indels

0; Mismatches

9; Conservative

Matches

Query Match Best Local Similarity

58 VLVNERWYL 66

1 VLVNERWVL 9

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58 VLVNERWVL 66
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potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (Kirx) and is used in the development of the transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                           Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                      SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 58-59; 74pp; English.
                       ABB84406 standard; protein; 253 AA.
                                                                                                                                                                                                                          08-FEB-2002; 2002WO-IB001300.
                                                                                                                                                                                                                                            09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
                                                               08-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                         gelrud T, Hansson L;
                                                                                                                                                                                                                                                                                                                               WPI; 2002-643380/69.
                                                                                   Human SCCE protein.
                                                                                                                                                                                                                                                                            (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 253 AA;
                                                                                                                                                                                 WO200262135-A2.
                                                                                                                                                                                                     15-AUG-2002.
                                            ABB84406;
RESULT 14
BBB84406
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Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease; metabolic disorder; inflammatory disorder; nervonal system disorder, sexual dysfunction, pain; mood disorder; hypertension, psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                     Whyte D, Sudarsanam S, Manning G, Caenepeel S;
                                                                                                                                                   Amino acid sequence of novel human protease #39.
                                                                                                                                                                                                                                      ocular disease; cytostatic; enzyme.
                                                                                AAU82740 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                   26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                                                                                                                                                          26-JUN-2000; 2000US-0214047P.
                                                                                                                             23-APR-2002 (first entry)
                     58 VLVNERWYL 66
1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-139913/18.
                                                                                                                                                                                                                                                                                                                                                                                 (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK31782
                                                                                                                                                                                                                                                                                    WO200200860-A2.
                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   Charydczak G;
                                                                                                                                                                                                                                                                                                           03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders.
                                                                                                      AAU82740;
                                                                     AAU827
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory diseases, merabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic chisorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, pain, sexual dysfunction, mood disorders at the disorders, neurological disorders, hypertension, psychotic disorders, neurological disorders, hypertension, psychotic disorders, neurological disorders (e.g. disease) and dyskinesias; The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. mineral professes (e.g. disease) and accular disease (e.g. disease). human proteases of the invention

Claim 6; Fig 2N; 313pp; English.

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Sequence 253 AA;
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0; Gaps
100.0%; Score 47; DB 5; Length 253; 100.0%; Pred. No. 2.5; cive 0; Mismatches 0; Indels
                  Local Similarity 100.0%;
les 9; Conservative C
  Query Match
                                         Matches
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1 VLVNERWVL 9 à

0; Gaps

Ouery Match 100.0%; Score 47; DB 5; Length 253; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 9; Conservative 0; Mismatches 0; Indels

58 VLVNERWVL 66

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March 1, 2004, 17:35:01; Search time 24.1111 Seconds (without alignments) 78.818 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
9: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
10: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
11: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
12: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
13: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
14: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
14: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
15: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
16: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
17: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
18: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
19: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 809742 seqs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .nimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                  US-09-905-083-34
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                      ile:
rfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oring table:
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Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 34, Appl Sequence 34, Appl	Sequence 98, Appl	Sequence 3, Appli	Sequence 90, Appl	Sequence 498, App	Sequence 48, Appl	Sequence 40, Appl	Sequence 50, Appl	Sequence 40, Appl	Sequence 50, Appl	Sequence 6, Appli	Seguence 7, Appli	Sequence 57, Appl	Sequence 8, Appli
SUMMARIES	US-09-918-243-34 US-09-905-083-34	US-09-888-615-98	US-09-764-762-3	US-10-264-283-90	US-10-295-027-498	US-10-173-999-48	US-09-918-243-40	US-09-918-243-50	US-09-905-083-40	US-09-905-083-50	US-10-202-676-6	US-10-045-367A-7	US-10-170-789-57	US-09-796-294-8
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% Query Match Length DB	9 9	253	253	253	253	253	6	თ	σ	6	228	81	81	260
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	91.5	91.5	91.5	91.5	83.0	80.9	80.9	80.9
Score	47	47	47	47	47	47	43	43	43	43	ъ Ф	38	38	38
Result No.	42	ო	4	ហ	φ	7	80	ማ	10	77	12	13	4.	15

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14 US-10-461-787-6 15 US-10-369-433-5000 15 US-10-156-214A-270 9 US-09-755-016-6 10 US-08-88-88-88-88-88-88-88-88-88-88-88-88-	US-10-017-610A-1 US-10-006-063A-1
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0.000000000000000000000000000000000000	9.9
	9 9 M M
H H H H H G G G G G G G G G G G G G G G	4.4 5.0

### ALIGNMENTS

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Sequence 34, Application US/09918243

Sequence 34, Application US/09918243

Sequence No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alesandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6233CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

PRIOR FILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 34

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Residues 58-66 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 47; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/09905083; Parent No. US20020146708A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLVNERWYL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-905-083-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-918-243-34
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CITY: Palo Alto

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PPLICANT: O'Brien, Timothy J.

ITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of
TILE OF INVENTION: Overlan Ceneral
TILE OF INVENTION: Overlan Ceneral
TILE REPRENCE: D6223GIP/C/Div
TILE REPRENCE: D6233GIP/C/Div
UNRENT APPLICATION UNMER: US 0/9/905,083
SRIOR APPLICATION UNMER: US 09/502,600
SRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
EQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 47; DB 9; Length 253; 100.0%; Pred. No. 2.9; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 47; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 7.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 58-66 of the SCCE protein
09-905-093-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09764762

Ratent No. US202006331A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER Drive
STREET: 3174 PORTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98, Application US/0988615
Patent No. USZ0020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CHARPEEL, SAN
APPLICANT: CHARPEEL, SAN
APPLICANT: CHARPEEL, SAN
APPLICANT: CHARPEEL, SAN
APPLICANT: SUDARSANAW, GIGEN
APPLICANT: SUDARSANAW, GIGEN
APPLICANT: SUDARSANAW, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
FRIOR APPLICATION NUMBER: US/09/88,615
CURRENT FILING DATE: 2001-06-26
FRIOR APPLICATION NUMBER: 60/214,047
SOFTWARE: PAROFILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SSOFTWARE: PAROFILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SSOFTWARE: PAROFILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SSOFTWARE: PAROFILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SSOFTWARE: PAROFILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
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Best Local Similarity 100.0
Matches 9; Conservative
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US-09-888-615-98
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VLVNERWYL 66
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US-09-764-762-3
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UK-10-264-283-90

(S-10-264-283-90)

(S-10-264-283-
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indele C
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                               COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-7a-2001
CILASSIFICATION NUMBER: 09/210,084
APPLICATION NUMBER: 09/210,084
FILING DATE: COMPONER: 09/210,084
FILING DATE: COMPONER: 09/210,084
FILING DATE: COMPONER: 09/210,084
FILING DATE: LOY 0:
MAME: Billings: LUCY 0:
REGISTRATION NUMBER: 36,749
REPERRENCE/COCKET NUMBER: PF-0252 US
TELECHMUNICATION IMPORMATION:
TELEPHONE: 415-845-0556
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERITICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S8 VLVNERWVL 66
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; ORGANISM: Homo sapiens
US-10-264-283-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 VLVNERWYL 66
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                                              ZIP: 94304
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PRIOR FILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: US 60/315,287
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
NUMBER: OF SEQ ID NOS: 163
SEQ ID NO 48
LENGTH: 253
LENGTH: 253
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 VLVNERWYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-243-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                            PEDLICANT: Afar, Daniel
PEDLICANT: Afar, Daniel
PEDLICANT: Afar, Daniel
PEDLICANT: Ginsberg, Wendy M.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Markey Richard
APPLICANT: Markey Richard
APPLICANT: Was Boot-0.25800US
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/85,733
PRIOR PEDLICANTON NUMBER: US 60/35,394
PRIOR APPLICANTON NUMBER: US 60/335,394
PRIOR APPLICANTON NUMBER: US 60/335,394
PRIOR PELING DATE: 2001-11-29
PRIOR PLING DATE: 2001-10-9
PRIOR PLING DATE: 2002-10-9
PRIOR PLING DATE: 2002-10-9
PRIOR PLING DATE: 2002-02-10
PRIOR PLING DATE: 2002-02-10
PRIOR APPLICATION NUMBER: US 60/35,250
PRIOR PLING DATE: 2002-02-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PLING DATE: 2002-02-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PLING DATE: 2002-02-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PLING DATE: 2002-02-13
PRIOR APPLICANTON NUMBER: US 60/355,250
PRIOR PLING DATE: 2002-02-13
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APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE REFERENCE: 018501-002420US
CURRENT APPLICATION WUMBER: US,100,173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION WUMBER: US 60/299,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 47; DB 15; Length 253; 100.0%; Pred. No. 29; Live 0; Mismatches 0; Indels 0; Gaps
                                                        quence 498, Application US/10295027
blication No. US20030232350A1
NERAL INFORMATION:
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Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
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Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-10-295-027-498
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LT 6
0-295-027-498
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Sequence 40, Application US/09918243

Sequence 40, Application US/09918243

Patent No. US20020142317A1

SEMERAL INFORMATION: Timothy J.

APPLICANT: Canton, Martin J.

CURRENT APPLICATION UNMER: US.

CURRENT APPLICATION UNMER: US.

PRIOR APPLICATION UNMER: US.

PRIOR APPLICATION UNMER: US.

PRIOR APPLICATION UNMER: US.

SEQ ID NOS: 136

LENGTH: 9
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Aleasandro
TITLE OF INVENTION: Methods for the
FILE REPRENCE: D6223CIP(C/D/CIP
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 101-07-13
WUMBER OF SEQ ID NOS: 136
SEQ ID NO 50
Query Match 100.0%; Score 47; DB 15; Length 253; Best Local Similarity 100.0%; Pred. No. 2.9; Matches 9; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
91.5%; Score 43; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: US/09/905,080
PRIOR APPLICATION NUMBER: 2001-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: OVARIAN CANCER
FILE REPERENCE: D6223CIP/Chiv
CURRENT APPLICATION WINERS: US/09/905,083
PRIOR APPLICATION WUMBER: US/09/905,000
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 50
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                                                                                    NAME/KEY: CHAIN
OTHER INFORMATION: Residues 59-67 of the SCCE protein
09-918-243-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 57-65 of the SCCE protein US-09-905-081-40
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US-09-068-083-50
IS-09-906-083-50
; Sequence 50, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-905-083-40
Sequence 40, Application US/09905083
Patent No. US20020146708A1
PERNENAL INPORMATION:
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ORGANISM: Homo sapiens
           TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 9
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91.5%; Score 43; DB 9; Length 9;

Query Match

NAME/KEY: CHAIN
OTHER INFORMATION: Residues 59-67 of the SCCE protein US-05-055-083-50

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MESUL: Application US/10202676
Sequence 6, Application US/10202676
Publication No. US2030092620A1
GENERAL INFORMATION:
APPLICANT: Lucas, John
APPLICANT: Briggs, Kristen
TITLE OF INVENTION: USE OF ADDPSIN/COMPLEMENT FACTOR D IN THE TREATMENT OF METABOLIC
TITLE OF INVENTION: RELATED DISORDERS
FILE REFRENCE: 121.US2.REG
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/308,147
PRIOR PELING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 6
SOOTHARE: REALERQ FOR Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
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Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
Best Local Similarity 100.0%; Pred. No. 7.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LOCATION: 27
COTHER INFORMATION: Polymorphic amino acid Ala or Gly
FORTHER:
NAME/KEY: VARIANT
LOCATION: 34
FORTURE:
FEATURE:
FEATURE:
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100CATION: 125
COTHER INFORMATION: Polymorphic amino acid Val or Leu
US-10-202-676-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT EXPELIES THE RESERVENT RESERVENT TITLE OF INVESTION: 14089, A NOVEL HUMAN TRYPSIN STITLE OF INVESTION: 14089, A NOVEL HUMAN TRYPSIN STITLE OF INVESTION: 14048-10901.
CURRENT APPLICATION NUMBER: US/10/045,367A.
CURRENT FILING DATE: 2002-04-15.
PRIOR APPLICATION NUMBER: 60/246,561.
PRIOR FILING DATE: 2000-11-07.
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FREUSEQ for Windows Version 4.0
LENGTH: 81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10045367A; Publication No. US20020165152A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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1 Mar 3 07:49:11 2004
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ö 0; Gaps APPLICANT: ROLAGE E. Meyers
APPLICANT: Clandt beter 7.
APPLICANT: APPLICANT: Mark
APPLICANT: Maine Mark
APPLICANT: Weich, Maine
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
TITLE OF INVENTION: NOVEL HUMAN PROTEIN COURSEST THEREOF
TITLE OF INVENTION: NOVEL TO 00.797, 039
BRIDG APPLICANTON WOMER: US 09/991, 049
BRIDG APPLICANTON WOMER: US 09/991, 046
BRIDG APPLICANTON WOMER: US 00.00-6.508
BRIDG APPLICANTON WOMER: US 00.00-6.709
BRIDG APPLIC 80.9%; Score 38; DB 13; Length 81; 75.0%; Pred. No. 32; tive 2; Mismatches 0; Indels quence 57, Application US/10170789 ublication No. US20030180930A1 UNFORMATION: ry Match t Local Similarity 75.0° ches 6; Conservative 5 LINEOWVL 12 2 LUNERWYL 9 LT 14 0-170-789-57

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80.9%; Score 38; DB 14; Length 81;

Best Local Similarity 75.0%; Pred. No. 32;

Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'Esten, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REPERENCE: D6020CIP3
CURRENT APPLICATION NUMBER: US/09/796, 294
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/618,259
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 8
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION WIMBER: EVT/US01/07014
PRIOR FILING DATE: 2001-03-05
PRIOR PRICHED NUMBER: US 60/187,420
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FREELSEQ for Windows Version 4.0
EQUID NO 57
LENGTH: 81
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                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: consensus sequence US-10-170-789-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/03796294; Patent No. US20020037581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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ORGANISM: Mus sp.
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March 1, 2004, 17:21:01 , Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	1 0	۰	ent	tissue kallikrein	neuropsin - mouse	cal pr	ന	m.	ypsin (	chymotrypsin (EC 3	hypothetical prote		·rt	hypothetical prote		A22R protein - var		٠	cal		S S	(EC 3.4.2	(BC	(EC 3.4	E)	$\sim$		dH u	1	coagulation factor
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ribosomal protein hypotherical prote haptoglobin precur haptoglobin - chim haptoglobin - chim haptoglobin precur haptoglobin - blac haptoglobin - blac haptoglobin - chim haptoglobin - chim haptoglobin precur branched chain-ami coaqulation factor	acrosin (E. 3.4.7.1 hypothetical prote unknown protein [i probable membrane
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## ALIGNMENTS

RESULT 1 A5368 Serine proteinase SCCE precursor - human Nilternate names: stratum corneum chymotryptic enzyme Cipecies: Homo sapiens (man) Cipecies: Coloning, Septementary Cipecies: Coloning, Septementary A; Accession. A53968 A; Accession. Accession. Accession. Accession. Accession. Accession. Ac	RESULT 2 DBHU complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment) No.Alternate names: adipsin; C3 convertase activator C.Species: Homos sapiens (man) C.Species: Homos (man) C.Speci
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A;Map position: 1
A;Introns: 22/3; 51/2; 92/1; 297/1; 354/1
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A, Gene: CESP: C32E8.6
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Status: probliminary

Goldenie 19-44, CC, 46-48 cBAL>

Somener: Factor D cleaves factor B when the latter is complexed with factor C3b, activenestics.

Sometics: D cleaves factor B when the latter is complexed with factor C3b, activenestics.

Gene: GDB:DF

Cross-references: GDB:132645, CMIM:134350

Cross-references: GDB:13645, GDB:136450

Cross-references: GDB:136450

Cross-refere
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Affolecule type: protein
Affolecule type: protein
Affolecule type: protein consists of two chains, A and B, held together by disulfide bonds
CfComment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release 1
CfComment: Tissue kallikrein cleave Met-Lys and Arg-Ser bonds in kininogen to release 1
CfComment: Tissue kallikrein bomology
CfComment: Trypsin, homology
Fil-224 Domain: trypsin, homology CHRY.
Fil-224 Domain: trypsin homology CHRY.
Fil-224 Domain: autolysis loop
Fig-1-232/Product: tissue kallikrein chain B #status experimental <MPTB>
Fig-144,26-42,121-190,155-169,180-205/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                   ilecule type: protein state of 19.75, TH, 78, P, 80-83, XXXIIIE, 90-172,86-91,185-235, 7 state a few residues were assigned from the previously published sequence of Reid et a yata, T, 0da, O, Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya Immunol. 27, 637-644, 19.75 immunol. 27, 637-644, 19.75 immunol. 17, 637-644, 19.75 immunol. 17, 637-644, PMID: 90370044; PMID: 2395435
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Siste Allikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
Siste Allikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
Sisteriate names: glandular kallikrein; kininogenin
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 Hsequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A00938; A92895
R;Tschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, M.;
Adv. Exp. Med. Biol. 120, 245-260, 1979
A;Fille: The primary structure of porcine glandular kallikreins.
A;Reference number: A90015
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A;Residues: 1-49, GML/,53-134, D',136-156, H',158, 'B',160-224, 'B',226-232 <TSC>
A;Residues: 1-49, GML/,53-134, D',136-156, 'H',158, 'B',160-224, 'B',226-232 <TSC>
A;Rode, W:, Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H.
J. Mol. Biol. 164, 237-282, 1983
A;Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein A, K.; structure and its comparison whith bovine trypsin.
A;Reference number: A2895; MUID:83189107; PMID:6551452
A;Contents: X-ray crystallography, 2 angstroms
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88.9%; Pred. No. 7.5;
tive 0; Mismatches 1; Indels
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Best Local Similarity 86.7.
Best Local 8; Conservative
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F.41,89,184/Active site: His, Asp, Ser #status experimental F.25/Binding site: carbohydrate (Asn) (covalent) #status experimental F.225/Binding site: carbohydrate (Asn) (covalent) #status experimental (Covalent) #status experimental (Covalent) (Bartial) #status experimental
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A;Accession: T25594
A;Actaus: preliminary; translated from GB/EMBL/DDBJ
A;Actaus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-417 <GAT>
A;Residues: 1-417 <GAT>
A;Experimental source: EMBL:U88308; PIDN:AAB42324.1; GSPDB:GN00019; CESP:C32E8.6
A;Experimental source: strain Bristol N2; clone C32E8
A;Genetics:
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25594
R;Gattung, S.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid G32E8.
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Pred. No. 12;
1; Mismatches 1; Indels
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Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels
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Chymotrypain (EC 3.4.21.1) 1 precursor - African malaria mosquito

Chymotrypain (EC 3.4.21.1) 1 precursor - African malaria mosquito

Chymotrypain (EC 3.4.21.1) 1 precursor - African malaria mosquito)

Chymotrypain (EC 3.4.21.1) 1 precursor - African malaria mosquito)

Chymotrypain - Amy-2000

Chacesian - Amy-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

Chymotry - Amy-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

Chymotry - Amy-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

Chymotry - Amy-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

R.Mustler In the EMBL Data Library, November 1992

A.Mocesion: Chaning of blood meal induced serine protease genes of the mosquito Any-Bescription: Chaning of blood meal induced serine protease genes of the mosquito Any-Bescription: Chaning of blood meal induced serine protease genes of two closely related Any-Bescription: Any-Coss-references: States and Chymotry April 19-May-2000

R.Wustler Any-Bescription: An Anopheles gambiae locus containing the sequences of two closely related Any-Bescription: An Anopheles gambiae locus containing the sequences of two closely related Any-Bescription: An Anopheles gambiae locus containing the sequences of two closely related Any-Bescription: Any-Bescribe and Any-Bescription: Any-Be
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C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999
C;Accession: T05892
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewe.
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    A, Cross-references: EMBL: Z18888; NID: 9509416; PIDN: CAA79326.1; PID: 9509417
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llarity 75.0%; Pred. No. 19;
Conservative 2; Mismatches 0; Indels
                                           C;Genetics:
A;Introns: 78/2; 209/3
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;1-17/Domain: aignal sequence #status predicted <SIG>F;18-32/Domain: activation peptide #status predicted <RC>F;33-258/Product: chymotrypsin 2 #status predicted <MAT>F;33-258/Product: chymotrypsin 2 #status predicted <MAT>F;59-75,182-198,208-232/Juliide bonds: #status experimental
F;74,19,212/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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lecies: Pleuronectes platessa (plaice)
lite: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Jul-1999
cession: T01779
aver, M.J.; George, S.G.
nitted to the EMBL Data Library, March 1996
serence number: Z14422
cession: T01779
tatus: preliminary; translated from GB/EMBL/DDBJ
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Specials: Pleuronectes placessa (plaice)

Sacession: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jul-1997

Accession: 531384

Fleaver, M.J. George, S.G.

Landmitted to the RMBL Data Library, November 1990

Reference number: 830567
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Crosb-references: EMBL:232645; NID:9474026; PIDN:CAAB3567.1; PID:9474027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.7%; Score 37; DB 2; Length 250;
66.7%; Pred. No. 18;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    ross-references: EMBL:X56744; NID:g1213630; PID:g64240

uperfamily: trypsin, trypsin, homology

esywords: hydrolase; protein digestion; serine proteinase

i3-242/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V,Cross-references: EMBL:XS6744
S,Supertamily: trypsin; trypsin; trypsin digestion; serine proteinase
S;28-words: bydrolase; protein digestion; serine proteinase
F;28-242/Domain: trypsin homology <TRY>
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ses 6; Conservative
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Sest Local S
Watches 6
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hypothetical protein A21R - variola major virus
CjSpecies: variola major virus
CjAccession: T28563
Rymasing, R.F.: Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin, Nature 366, 748-751, 1993
A;Tile: Potential virulence determinants in terminal regions of variola smallpox virus 5
A;Reference number: Z20488; MUID:9408847; PMID:8264798
A;Recession: T28563
A;Rocession: T28563
A;Rocession: T28563
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-426 cMRS
A;Residues: 1-426 cMRS
A;Residues: L426 cMRS
A;Residues: references: EMBL:122579; NID:9622595; PIDN:AAA60873.1; PID:9439043
A;Croserimental source: strain Bangladesh-1975
C;Superfamily: vaccinia virus probable 49.1K protein
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jate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
Accession: C36850
A,Reference number: A45161; MUID:93077530; PMID:1447189
A,Accession: A45161
A,Status: prefilminary
A,Molecule type: mRNA
A,Residues: 1-238 -63N2>
A,Cross-references: GR:U05175; NID:9206691; PIDN:AAA42056.1; PID:9206692
C,Superfamily: trypsin homology
C,Reywords: hydrolase; serine proteinase
F;21-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:X69198, NID:g456758; PIDN:CAA49065.1; PID:g297303
C;Superfamily: vaccinia virus probable 49.1K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.6%; Score 36; DB 2; Length 426; llarity 55.6%; Pred. No. 49; Conservative 3; Mismatches 1; Indels
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Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels
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R.Blinov, V.M.
Bubmitted to Genbank, November 1992
A. Reference number: A36859
A. Accession: C36850
A. Accession: C36850
A. Molecule type: DNA
A. Residues: 1-426 ABLIS
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Matches
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C72166
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A45161
E;Smyth, M.J.; Wilrrout, T.: Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.;
J. Biol. Chem. 267, 24418-24425, 1992
A,Tutle Purification and cloning of a novel serine protease, RNK-Met-1, from the granul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: F82825
annoymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
sture 406, 151-157, 2000
Title: The genome sequence of the plant pathogen Xylella fastidiosa.
Reference number: A82515; MUID:20365717; PMID:10910347
Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ap position: 5
Tatrons: 72/3; 142/3; 227/2; 344/3; 372/3; 941/2; 1016/3; 1038/3; 1055/1; 1095/2; 1155
ote: F6H11.110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pothetical protein XF0279 [imported] - Xylella fastidiosa (strain 9a5c)
Species: Xylella fastidiosa
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.7%; Score 37; DB 2; Length 1421; 66.7%; Pred. No. 1.1e+02; tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                       perimental source: cultivar Columbia; BAC clone F6H11
anetics:
                              itted to the Protein Sequence Database, April 1998 [ference unuber: 215456 cession: 105892]. Ilecule type: DNA sidues: 1-1421 aBBV sidues: 1-1421 aBBV aldues: 1-1421 
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Best Local Similarity 62.5*
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A45161
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0; Gaps

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protein - variola minor virus (strain Garcia-1966)
ecies: variola minor virus
tes: 24.Nov-1999 #text_change 20-Jun-2000
cession: C72166
ichelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
scription: Analysis of the complete coding sequence of DNA of alastrim variola minor
scription: Analysis of the complete coding sequence of DNA of alastrim variola minor
scription: Analysis of the complete coding sequence of DNA of alastrim variola minor
scession: C72166
catus: preliminary
cleanis preliminary
catus: preliminary
cation: 76.6%; Score 36; DB 2; Length 426;
catus: preliminary
catus: preliminary
catus: prediminary
catus: propagation
catus: prediminary
catus:
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yarch completed: March 1, 2004, 17:36:28
yb time : 10.3333 secs

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March 1, 2004, 17:20:41; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                       protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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sp_vertebrate:*
sp_unclassified:*
sp_tvirus:*
sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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rfect score:
quence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8n5n9 homo sapien	O9ffr7 arabidopsis	Q9myv8 bos taurus	Q8jfq7 gadus morhu	Q9xy58 ctenocephal	Q7sze2 agkistrodon	Q7z0g5 phlebotomus	Q8t3b8 caenorhabdi	Q9sny8 solanum tub	Q9sny9 solanum tub	P91123 caenorhabdi	Q9pt51 agkistrodon	Q8uuj1 agkistrodon	O9vem7 drosophila	Q9w6k0 notothenia	092046 dissostichu
SUMMAKES	αī	Q8N5N9	Q9FFR7	Q9MYV8	Q8JFQ7	Q9XY58	Q7SZE2	Q7Z0G5	Q8T3B8	QSSNY8	6 ANS60	P91123	Q9PT51	Q8UUJ1	Q9VEM7	Q9W6K0	092046
	DB	4	10	v	13	S	13	Ŋ	Ŋ	10	10	Ŋ	13	13	Ŋ	13	13
	% Query Match Length DB	253	455	100	249	223	234	262	313	377	418	461	233	234	243	249	249
	% Query Match	100.0	85.1	83.0	83.0	80.9	80.9	80.9	80.9	80.9	6.08	80.9	78.7	78.7	78.7	78.7	78.7
	Score	47	40	39	39	38	8	38	38	38	38	38	37	37	37	37	37
	Result No.	н	7	m	4	S	y	7	80	Q	10	11	12	13	14	15	16

093265 pseudopleur 097098 anopheles a 097100 anopheles d 09ptl3 agkietrodon 09ygj9 agkietrodon	·	Q86ws5 homo sapien Q9w6j8 dissostichu Q98ik4 thizobium I Q9pq19 xyleila fas	Q9ukr2 homo sapien O45048 anopheles g Q98n76 rhizobium l Q9v887 drosophila Q923y5 rattus norv		Q9j193 ectromelia Q89166 variola vir Q80hv4 vaccinia vi Q80dv4 cowpox viru
13 093265 5 097098 5 097100 13 09FTL3 13 09YGJ9	5 Q9XY53 13 Q7SZE1 13 Q8UUK2 13 Q8QHK3 13 O9W6J9	4 Q86WS5 13 Q9W6J8 16 Q98IK4 16 Q9PGL9	00 0	16 098413 12 057228 12 094780 12 084284 12 080404	12 08J193 12 089166 12 080HV4 12 080DV4
2225 225 237 237 237 242 242 242 242 242 242 242 242 242 24	2 2 2 2 2 2 3 8 8 2 2 3 8 8 8 8 9 2 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	348 675 1176 72	111 255 295 349	6 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6	4444 00000 0000
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## ALIGNMENTS

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0; Gaps
                                                                                           01-OCT_2002 (TrEMBLrel. 22, Created)
01-OCT_2002 (TrEMBLrel. 22, Last sequence update)
01-OCT_2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 7 (chymotryptic, stratum corneum).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.
NOBI_TAXID=9606;
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Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                       253 AA.
                                                                       PRT;
                                                                       PRELIMINARY;
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                                                                   GNSN80
RESULT 1
                                   6NSN80
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SEQUENCE
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Q9XY58
ID Q9XY58
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Matches
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MEDLINE-97417969; PubMed-9330910;
MEDLINE-97417969; PubMed-9330910;
MEDLINE-97471969; PubMed-9330910;
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned pl clones."
DNA Res 4:421-2230 (1997).
EMBL; AB005233; BAB11469.1; -.
InterPro; IPR001810; F-box.
InterPro; IPR001810; F-box.
InterPro; IPR00845; Skpl_Skp2.
Pfam; PF00646; F-box: 1.
Pfam; PF00646; F-box: 1.
Pfam; PF00646; F-box: 1.
                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, Pl clone:MBK23.
Arabidopsis thallana (Mouse-ear oress).
Eukaryoca, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
NCBL TaxID=3702;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammanlia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
MCBI_TaxID=9913;
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Lavery K.S., Galler C., Killian G.J.;
Lavery K.S., and localization of haptoglobin in the bovine female reproductive tract.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ7115; CRC00531.1; -.
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OS. GO:000823; F:peptidase activity; IEA.
GO; GO:000823; F:trypsin activity; IEA.
GO; GO:0006508; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
Pfam; PF00089; trypsin; 1.
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Last annotation update)
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                          58 VLVNERWYL 66
     1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Meopterygii; Teleostei; Euteleostei; Mooteleostei;

Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
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"Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group.",
"Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group.",
"Solution of Salary Section Of Salary Section
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                  Score 39; DB 6; Length 100;
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Pyloric caecum;
Gudmundsdottir A.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 AA; 27400 MW; 8FB98462CEDBEFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *O8JFQ7 PRELIMINARY; PRT; 249 AA. 08JFQ7; 010-007-2002 (TERMELrel. 22, Created) 01-007-2002 (TERMELrel. 22, Last sequence update) 01-007-2003 (TERMELrel. 25, Last annotation update) Trypsingen Y precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.

PRINTS; PR0022; CHNOTRYPSIN.

SNART; SN00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SRF; 1.

Hydrolase; Protease; Serine protease; Signal.

SIGNAL
83.0%; Scc. 75.0%; Pred. No. b.r. 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSINGEN Y.
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                                                             Local Similarity 75.0
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TISSUE=Pyloric caecum;
PubMed=10612685;
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249 249
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22 LINERWLL 29
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Best Local Similarity
Matches 6; Conserv
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20 VLINDOWVL
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30 LVNEEWVL 37

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TISSUE-Midgut;
Ramalho-Ortigao M., Kamhawi S., Rowton E., Sacks D.L., Ribeiro J.M.,
Valenzuela J.G.; Valenzacterization of trypsins and chymotrypsins-like
Proteases from the midgut of the sand fly vector Phlebotomus
paparasi.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY128106; AAM96338.1;
SEQUENCE 262 AA; 28863 MW; 31F11012206A65D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                Phlebotomus papatasi.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopter-Ygota, Diptera, Nematocera, Psychodoidea;
Psychodidae, Phlebotomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.9%; Score 38; DB 5; Length 262; 75.0%; Pred. No. 35; ive 2; Mismatches 0; Indels
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STRAIN=Bristol N2;
Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; 188308, AAM15557.1; -.
WormPep; C32E8.6b; CE30371.
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                       01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
Waterston R.;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
C32E8.6.
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Best Local Similarity 75...
6; Conservative
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                                                                                                                            PRELIMINARY;
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57 ILNERWVL 64
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                                                                                                                                                                                                                                                        Chymotrypsin.
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                                                              RESULT 7
Q7Z0G5
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                                                                                                                                                                                                                                                                                           075ZE2;
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last annotation update)
Thrombin-like enzyme defibrase (Fragment).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chymotrypsin-like serine protease (Fragment).
SP-4.
Ctenocephalides felis (Cat flea).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Siphonaptera, Pulicidae,
Ctenocephalides.
NEBL TaxID=7515;
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87.5%; Pred. No. 31;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 38; DB 5; Length 223; 75.0%; Pred. No. 29; tive 2; Mismatches 0; Indels
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Sun D.-J., Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY204242; AAP2037.1; -.
NON TER 1
SEQUENCE 234 AA; 25351 MW; 0124C1485525F560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA; 24844 MW; C34EBE9455DD7DE9 CRC64;
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NON TER
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Best Local Similarity 87.5'
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Best Local Similarity 75.0
Matches 6; Conservative
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SEQUENCE FROM N.A.
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7SZE2
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2 LUNERWUL 9

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P91123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROW N.A.
STRAIN-cv. Russet Burbank;
STRAIN-cv. Russet Burbank;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
Clashell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
Clashell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
aminotransferase from potato.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1934646, AR07192.1;
HSSP: P00510; 1A346.
                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Solanum tuberosum (Potato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                      Score 38; DB 5; Length 313;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIMEY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransferase (EC 2.6.1.42).
                                                                                                                                                                                                                                                                                                            QSNY9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransferase (EC 2.6.1.42).
                                                                                                                                                        0; Indels
                                                                                            35608 MW; 4372ED66478E434A CRC64;
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                                                                                                                                                        1; Mismatches
GO, GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA..
Interpro; IPR00873; AMP-bind.
Pfam; PF00501; AMP-binding; I.
Fram; PF00501; AMP-binding; I.
Hypochetical protein.
ERQUENCE 313 AA; 35608 MW; 4372ED66478
                                                                                                                        Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                         ||:|||
219 VLINERW 225
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                                                                                                                                                                                    1 VLVNERW 7
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9SNY9
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                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. Russet Burbank;
STRAIN=cv. Russet Burbank;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
"Isolation of a functional gene encoding for branched-chain amino acid aminotransferase from potato.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF193845; AAF07191.1; ---
HSSP; P00510; IA3G.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 10; Length 418;
Pred. No. 57;
1; Mismatches 1; Indels
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"Direct Submission.";
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 188308, AAB42344.2;
PIR; T25594; T25594.
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"The sequence of C. elegans cosmid C32E8.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45296 MW; E6EA6C2B3A58C814 CRC64;
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Last annotation update)
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WormDep, C3288 dea, CE27814.
WormDep, C00:0003824; F:catalytic activity; IEA.
GO; GO:0008125; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000873; AMP-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
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VLANERWI 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLVNERWV 8
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Best Local Similarity
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Thrombin-like enzyme ussurase (Fragment)
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Q9VEM7
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MEDLINE=20302322; PubMed=10845699;

MEDLINE=20302322; PubMed=10845699;

Lee J.W., Park W.J.

Lee J.W., Park W.J.

Lee J.W., Park W.J.

Lenzyme from Agkistrodon blomboffii brevicaudus snake venom, by serial hybridization-polymeras e chain reaction.";

Arch. Biochem. Biophys. 377:234-240(2000).

L. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

RESP. P00763; 1DPO.

MEROPS; S01.185; ...

MEROPS; S01.184; Peptidase S1A.

MEROPS; MEROPS; MEROPSIN; ...

MEROPS; MEROPS; MEROPSIN; MEROPSIN; MEROPS; ...

MEROPS; MEROPS; MEROPSIN; MEROPSIN; MEROPSIN; MEROPSIN; MEROPSIN; MEROPSIN; MEROPS; MEROPSIN; MEROPS; MEROPSIN; MERO
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                                                                                                                                                            Gaps
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Agkietrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).

Agkietrodon halys blomhoffi (Mamushi) (Strebrata; Buteleostomi;
Lebidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
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                                                                                                              80.9%; Score 38; DB 5; Length 461;
85.7%; Pred. No. 63;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AA; 25725 MW; 1676DC5AF0AB5A42 CRC64;
  Pfam; PF00501; AMP-binding; 2.
PROSTE; P800455; AMP_BINDING; 1.
Hypothetical protein.
SEQUENCE 461 AA; 51902 MW; 8662F7486A0E57A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta-fibrinogenase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Protease; Serine protease.
NON TER 1
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QBUUJI;
01-MAR-2002 (TEMBLrel. 20,
01-MAR-2002 (TEMBLrel. 20,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                      Query Match 80.9%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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219 VLINERW 225
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                                                                                                                                                                                                          1 VLVNERW 7
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GTRAINSEBERKELEY,

KENDLINES-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Abhburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Ann K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxmadale J., Bayraktaroglu L., Beasley E.M.,

Beson K.Y., Banos P.V., Berman B.P., Blandari D., Bolahakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Poison gland;
Daolin D., Xiaodong D., Wenfang W., Anguo L., Mei X.;
Daolin D., Xiaodong D., Wenfang W., Anguo L., Mei X.;
"Cloning and Sequence Analysis of CDNAs for Thrombin-like Enzymes,
"Cloning and Sequence Analysis of CDNAs for Thrombin-like Enzymes,
USSUIIN and USBUIASSE, From Agkistrodon halys ussuriensis Snake
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Gloydius.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG4053 protein.
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Best Local Similarity 75.0
Matches 6; Conservative
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de Pablos B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M.,
Dodson K., Doup i.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn D.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Tosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Gran P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hermadez J.R., Houck J.,
A Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
Jalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y. Leviteky A.A., Li J. Li Z., Liang Y., Lin Z.,
Lasko P., Lei Y. Leviteky A.M., Mill J. Li Z., Liang Y., Lin Z.,
Nalani M., Moy M., Murphy B., Morris J., Moshrein D.L.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreif A.,
Nerkulov G., Milshina N.V., Mobarry C., Morris J., Poslon D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Rainer K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Milliams S.M., Woodage T., Weinstock G.M., Weiseenbach J.,
Milliams S.M., Myers E.W., Rubin G.M., Venter E., Wang S., Yao Q. A.,
Milliams S.M., Myers E.W., Rubin G.M., Venter J.C.;
Milliams S.M., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
Schence 287:2185-2195(2000).
Handel A. Myers B. M., Myers B. M., Marker B. M., Melby, Romer B.,
Bendling A.C., Stapleton M., Strong K., Smith H.O.,
Rembl., Arborg F. W., Rubin G.M., Venter J.C.;
Rembl., Arborg T. W., Staple M., Staple M.,
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 12, Last annotation update)
1-OCT-2003 (TrEMBLre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 5; Length 243;
Pred. No. 50;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0722; CHYMOTRYBSIN.
SMART; SMOSO20; TRYPSIN BPC; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN BS; 1.
PROSITE; PS00135; TRYPSIN BS; 1.
PROSITE; PS00136; TRYPSIN BS; 1.
SEQUENCE 243 AA; 26992 MW; 393C4B710563C811 CRC64;
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60:0008233; F:peptidase activity; IEA.
GO:0004295; F:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysi
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
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GO; GO:0004263; F:chymotrypsi
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Best Local Similarity 55.6
Matches 5, Conservative
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                                                                                                                                                                                                                                                             MEROPS; SO1.124; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008333; F:peptidase activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
                                                               SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
L; AF134323; AAD30107.1; -.
P; P00761; 1EPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001254; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
Pfan, PF00089; trypain; 1.
Pfan, PF00089; trypain; 1.
PRNITS; PR00722; CHYMOTRYPSIN.
SYART; PR00722; CHYMOTRYPSIN.
SYART; PR001125; TRYPSIN. DOM; 1.
PROSITE; PS00240; TRYPSIN. DOM; 1.
HYGLOLASS; TRYPSIN. SER; 1.
HYGLOLASS; TRYPSIN. SER; 1.
HYGLOLASS; PROTESSIN. SER; 1.
SEQUENCE 249 AA; 27419 MW; 69C0D872
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Best Local Similarity
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NCBI_TaxID=9606;
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KLK7 H.
P49862;
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                                                                        Description
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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NEN ROLE
NRPN RAT
NEN PLEBL
VSP4 TRIMU
VSP5 TRIMU
VSP6 TRIMU
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TEST_MOUSE
HPT_CANFA
                                                      protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
42-2003 (Rel. 42, Last annotation update)
enzyme) (hSCCE).
KLK7 OR PRSS6 OR SCCE.
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE FROM N.A.

TISSUE=Keratinocytes;
Yousef G.M., Scorilas A., Diamandis E.D.;
"Molecular characterization, mapping and tissue expression of human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                     Q9m401
P00741
P10323
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P45900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                           HPT_PIG
HPTR HUMAN
HPT HUMAN
BCA3_ARATH
ASP BOVIN
C1S HUMAN
C1S HUMAN
VSPA_BACSU
VSPA_LACMU
VSPA_LACMU
VSPA_LACMU
VSP1_BOTUA
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MEDLINE=95314630; Pubmed=7794273;
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SEQUENCE
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-Tyr-26, and 26-Tyr-|-The-7. Could play a role in the activation of precursors to inflammarcry cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sus scrofa (Pig)
Sus scrofa (Pig)
Sus scrofa (Pig)
Sus scrofa (Pig)
Nordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TAXID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
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GO; GO: 0008544; P: epidermal differentiation; TAS.
InterPro; IPR001903; Cys_Ser_trypsin.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
Fram; PR00189; trypsin; 1.
FRINTS; PR00722; CTYPOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PHQLICAGES; Serine procease; Zymogen; Glycoprotein; Signal.
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EMBL, AF166330, AAD4918.1, --
EMBL, AF34527, AAG33360.1, --
EMBL, AF32583, AAK69624.1, --
PIR, A53968, A53968.
HSSP, P00763, 1DPO.
MEROPS, 501.300; --
Genew, HGNC 6368, KLK7.
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9; Conservative
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"Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein A, a specific trypsin-like serine proteinase. Crystallization, structure determination, crystallographic refinement, structure and lits comparison with bovine trypsin."; J. Mol. Biol. 164:237-282(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90336040; PubMed=2379280; Kamada M., Kizuki K., Moriya H., Kamada M., Ikekita M., Kurahashi T., Aoki K., Kizuki K., Moriya H., Swealey C.C., Kamo M., Tsugita A.; "Generation of a different type of beta-kallikrein from porcine pancreatic alpha-kallikrein by the action of chymotrypsin -observation of proteolytic processing occurring around 'kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PANCREATIC TRYPESION INTERIOR.
MEDLINE-83189108; PubMed-6188842;
MEDLINE-83189108; PubMed-6188842;
MEDLINE-83189108; PubMed-6188842;
MEdined 2.5 A X-ray crystal structure of the complex formed by porchine kallikrein A and the bovine pancreatic trypsin inhibitor.
Crystallization, Patterson search, structure determination,
Crystallization, Patterson search, structure determination,
bovine trypsin-pancreatic trypsin inhibitor complex.";
J. Mol. Biol. 164:283-311(1983).
                                                                                    "Generation of alpha- and beta-kallikreins from porcine pancreatic prokallikrein by the action of trypsin."; Chem. Pharm. Bull, 36:4891-4899(1988).
                                                                                                                                                                                                            Tschesche H., Mair G., Godec G., Fledler F., Ehret W., Hirschauer Lemon M., Fritz H., Schmidt-Kastner G., Kutzbach C.; "The primary structure of porcine glandular kallikreins."; Adv. Exp. Med. Biol. 120:245-260(1979)
                                                                                                                                                                                                                                                                                                                                                                  "The primary structure of the kallikrein from porcine pancreas."; Thesis (1976), University of Munich, Germany.
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MEDLINE-83189107; PubMed=6551452;
Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
                  SEQUENCE OF 1-15 AND 95-102.
MEDLINE-89230643; PubMed=3246048;
Kamada M., Aoki K., Ikekita M., Kizuki K., Moriya H., Kamo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE
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Fiedler F., Fink E., Tschesche H., Fritz H.;
"Porcine glandular kallikreins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. Pharm. Bull. 38:1053-1057(1990).
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                                                                                                                                                                          SEQUENCE OF 8-87 AND 95-246.
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  NRPN MOUSE
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R PDB; 2KX; 19-JUL-84.

R PDB; 1HIA; 24-DEC-97.

R MERCPES, SO1.160; 24-DEC-97.

R InterPro; 1PR001903; Cys Ser trypsin.

R InterPro; 1PR001914; Peptidase_S1.

R InterPro; 1PR001314; Peptidase_S1.

R PRINTS; PR00172; CHYMOTRYPSIN.

R SMART; SM00020; Tryp_SPC; 1.

R PROSITE; PS00134; TRYPSIN DOW; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R Hydrolase; Serine protease; Glycoprotein; Pancreas; 3D-structure;
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                                       Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G., Structure 5:585-585(1997).
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KALLIKREIN (AUTOLYSIS) LOOP.
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SEQUENCE FROM N.A.

STRAIM=CZech II; TISSUE=Manmary gland;

MEDINE=2238257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Keteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                Score 38; DB 1; Length 246;
Pred. No. 4.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7B4.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
27170 MW; 5991CEDE406A19A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q61955;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8)
KLK8 OR PRSS19 OR NRPN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluoride.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Expressed specifically in the limbic system of TISSUE SPECIFICITY: Expressed specifically in the limbic system of mouse brain and is localized at highest concentration in pyramidal neurons of the hippocampal CA1-3 subfields.

MASS SPECTROMETRY: NWw-26613; NETHOD=NALDI; RANGE=29-260.

MASS SPECTROMETRY: NWw-26229, METHOD=NALDI; RANGE=33-260.

MASS SPECTROMETRY: NWW-26229; METHOD=NALDI; RANGE=33-260.

MASS SPECTROMETRY: Ma-26229; METHOD=NALDI; RANGE=33-260.

SIMILARITY: Belongs to peptidase family S1. Rallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by dIIsopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hippocampus;
MEDLINE-99134351; PubMed=9933620;
KISHI T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
Shiosaka S., Hakoshima T.;
Shiosaka S., Hakoshima T.;
"Crystal structure of neuropsin, a hippocampal protease involved in
"Crystal structure of neuropsin, a hippocampal protease involved in
"Crystal structure of neuropsin, a hippocampal placticity. Has a strong proteolytic activity against
fibronectin.
                                                                                                                                          SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
MEDLINE-98225202; PubMed=955608;
Shiniatu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a
plasticity-related serine protease.";
U Biol. Chem. 273:11189-11196(1998).
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  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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R EMBL; D30785; BAA06451.1; ---
R EMBL; BC05895; AAH5895.1; ---
R EMBL; BC05895; AAH5895.1; ---
R PDB; INPM; 23-MAR-99.
R MEROPS; S01.244; ---
R MGD; MGI:892018; KIN8.
R INTECPRO; IPR001254; Peptidase_S1.
R INTECPRO; IPR001254; Peptidase_S1.
R INTECPRO; IPR001254; Peptidase_S1.
R PRINTS; PR00722; CHYMPYSIN.
R PROSITE; PS0240; TRYPSIN.
R PROSITE; PS0134; TRYPSIN DOM; 1.
R PROSITE; PS010134; TRYPSIN DOM; 1.
R PROSITE; PS010134; TRYPSIN DER; 1.
R PROSITE; PS010134; TRYPSIN SER; 1.
R PROCATE; PS010135; TRYPSIN SER; 1.
R PROCATE; PS010135; TRYPSIN SER; 1.
R PROCATE; PS010134; TRYPSIN SER; 1.
R PROCATE; PS010134; TRYPSIN SER; 1.
R PROCATE; PS010134; TRYPSIN SER; 1.
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Amamalia, Butharia; Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                             15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
15-UTL-1999 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).

KLK8 OR PRSS19 OR NRPN OR BSP1.
                             N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                            Length 260;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                            256
28523 MW; BESF6F6BE37CD60E CRC64;
                                                                                                                                                                                                                                                                                                            80.9%; Score 38; DB 1;
ilarity 77.8%; Pred. No. 4.5;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  260 AA
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61 VLVGDRWYL 69
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Best Local Similarity
7; Conserve
1 VLVNERWYL
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                   TISSUE=Liver;
Leaver M.G., George S.G.;
Leaver M.G., George S.G.;
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SUBCELLULAR Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 250;
Pred. No. 6.7;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637DE96185C1ABAA CRC64;
                                                                                                                                                                                                                                                                                                                                     HSSP; PUUVOL;

RICHEPRO; IPRO01254; Peptidase_S1.

READ: PRO0125; CHYMOTRYPSIN.

DR ROSITE; PSO0124; TRYPSIN DOM; 1.

DR PROSITE; PSO0134; TRYPSIN DOM; 1.

DR PROSITE; PSO0135; TRYPSIN HIS; FALSE_NEG.

DR PROSITE; PSO0135; TRYPSIN SER; 1.

FW Hydrolase; Serine protease; Symbol: Signal.

FT PROPEP 16 22 ACTIVATION PEPTIDE.

THYPSIN DOM: PROPIDE.
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Similarity 66.7%;
6; Conservative 2
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HSSP; P00761; 1EPT.
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1063
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Best Local Similarity
Matches 6; Conserv
 FROM N.A.
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                                                                                                                                                                                                        This SMISARITY: Belongs to peptidase family Si. Kallikrein subfamily.

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RYP PLEPL
D TRYP PLEPL
C P35034;
T 01-FEB-1994 (Rel. 28, Last sequence update)
T 01-FEB-1994 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
T Trypsin precursor (BC 3.4.21.4).
S Pleuronectes platessa (Plades) (Graniata; Vertebrata; Buteleostomi; C Actinopterygii; Neopterygii; Percomorpha; Acanthopterygii; Percomorpha; Peuronectides;
C Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectides;
C Pleuronectoidei; Pleuronectidae; Pleuronectes.
W NCBI TaxID=8262;
Gaps
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 38; DB 1; Length 260; llarity 77.8%; Pred. No. 4.5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS, S01.244; -...
MEROPS, S01.244; -...
InterPro; IPR0019003; Cys_Ser_trypsin.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IRR0010134; Peptidase_S1A.
Prim, PF000089; trypsin; 1.
PRINTS; PR000722; CHMOTRYPSIN.
SMART; PS00210; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
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HSSP; Q61955; 1NPM.
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Matches 7; Conserv
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SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE=95110313; PubMed=7811255;
MEDLINE=95110313; PubMed=7811255;
"Hung C.-C., Huang K.F., Chiou S.-H.;
"Characterization of one novel venom protease with beta-fibrinogenase
RESULT 6
VSP4_TRIMU

TIMU

COPICATION

CONTROL

TO COT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Mucrofibrase 4 precursor (EC 3.4.21..).

CO Trimeresurus mucrosquamatus (Taiwan habu).

CO Taiwaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CO Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

CO Viperidae; Crotalinae; Protobothrops.
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Gaps

SPECIFICITY (BY SIMILARITY)

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                       -!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
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  (Trimeresurus mucrosquamatus):
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MUCROPIBRASE
CHARGE RELAY SYSTEM (E
BY SIMILARITY.
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Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zymogen; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; 19R009003; Cys_Ser_trypsin.
InterPro; 19R001254; Peptidase_S1.
InterPro; 19R001254; Peptidase_S1A.
Pfan; Pr00089; trypsin; 1.
PRINTS; PR00122; CHYMCTRYPSIN.
SMART; SM00200; Tryp_Sro; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN LIS; 1.
Hydrolase; Serine protease; Zymogen; Signala.
                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
  the Taiwan habu
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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LINEEWVL 60
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     from
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D VSPS_TK1.
Q91511;
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"Characterization of one novel venom protease with beta-fibrinogenase activity from the Taiwan habu (Trimeresurus mucrosquamatus): purification and cDNA sequence analysis.";
Biochem Biophys. Res . Commun. 205:107-1715 (1994).
-!- FUNCTION: Thrombin-like snake venom serine protease. Cleaves beta-chain of fibrinogen molecules efficiently and shows relatively lower activity on alpha-chain, with almost no activity on gamma-
                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Protobothrops.
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 257; Pred. No. 6.9; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCCF64A8EAF2827D CRC64;
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16-00T-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Serpentokallikrein-2 precursor (EC 3.4.21.).
Trimeresurus mucrosquamatus (Taiwan habu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.78;
75.08;
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HSSP; P00763; 1DPO.
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102
257 AA;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=103944;
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VSP7 TK1..
ID VSP7 TR1:..
Q9DG84;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Mucrofibrase 5 precursor (EC 3.4.21.-).
Trimeresurus mucrosquamatus (Taiwan habu).
Itimeresurus Squamata; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae, Crotalinae; Protobothrops.

TISSUE=Venom gland; MEDLINE=95110313; PubMed=7811255; Hung C.-C., Huang K.F., Chiou S.-H.;

SEQUENCE FROM N.A.

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Japo3822, RAG7253.1;

Japo3822, RAG7253.1;

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Japo3822, RAG7253.1;

Interpro; IPRO00203; Cys Ser trypsin.

Interpro; IPRO00204; PRPSIN INTERPROSE

REMART; SWOO0207; Trypsin.

R RAINAT; SWOO0207; Trypsin.

R RAINAT; SWOO0207; Trypsin.

R RAINAT; SWOO0207; Trypsin.

R RAINAT; SWOO0207; Trypsin.

PROSTIE; PSO0134; Trypsin INCM; I.

PROSTIE; PSO0134; Trypsin INCM; I.

PROSTIE; PSO0135; Trypsin INCM; I.

PROSTIE; PSO0135; Trypsin INCM; I.

PROSTIE; PSO0134; Trypsin INCM; I.

PROSTIE; PSO0135; Trypsin INCM; I.

PROSTIE; PSO0136; Trypsin I
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
TLGCC.
TLGCC.
Trimeresurus gramineus (Indian green tree viper) (Green habu snake).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

IISSUE-Venom gland;
MEDLINE=97096898; PubMed=8941719;
Deshimaru M., Ogawa T., Nakashima K., Nobuhisa I., Chijiwa T., Shimohigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S., Oho,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 AA
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                                      Gaps
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Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
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N-LINKED (GLCNAC. .) (POTENTIAL).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR Rimits; PR001324; Peptidase_S1A.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00202; TRYPSIN_DM; 1.

PROSITE; PS00134; TRYPSIN_DM; 1.

PROSITE; PS00135; TRYPSIN_BER; 1.

R PROSITE; PS00135; TRYPSIN_BER; 1.

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1 25 257 VENOM SERTINE DECREE.
"Accelerated evolution of crotalinae snake venom gland serine
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Pred. No. 6.9;
1; Mismatches 1; Indels
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Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Suakoko; TISSUE=Midgut;
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ilarity 75.0%;
Conservative
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HSSP; P00763; 1DPO.
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257 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CHANGTRYPSIN 2.
CHANGE RELAY SYSTEM (BY SIMILARITY).
CHANGE RELAY SYSTEM (BY SIMILARITY).
CHANGE RELAY SYSTEM (BY SIMILARITY).
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SEQUENCE FROW N.A.
STRAIN-Suakoko, TISSUE-Midgut;
STRAIN-Suakoko, TISSUE-Midgut;
Mueller H.M., Catteruccia F., Crisanti A.;
Man Anopheles gambiae locus containing the sequences of two closely
related chymotrypsin-like proteases induced in the gut following blood
meal.";
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa,
-- TISSUE SPECIFICITY: Midgut.
-- TISSUE SPECIFICITY: Midgut.
-- DEVELOPMENTAL STAGE: Induced in the midgut of female after blood
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027289;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chymotrypsin 1 precursor (EC 3.4.21.1).
CHYMI.
Annopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_DM; 1.
PROSITE; PS00135; TRYPSIN_DER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal; Zymogen; Digestion; Multigene family.
Interprofit of the protease of the prote
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3H -> FPD (IN REF. 1).
A41AD20A630BC67B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to peptidase family S1.
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EMBL; Z32645; CAA83567.1; -.
PIR; S44184, S44184.
HSSP; PO0761; 1EFT.
MEROPS; S01.121; -.
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63 LLNDRWVL 70
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TR1 ANOGA
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SUBAKOKO; TISSUE-Midgut;
Mueller H.M., Catteruccia F., Crisanti A.;
"An Anopheles gambiae locus containing the sequences of two closely
related chymotrypsin-like proteases induced in the gut following blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                              "Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Pbe-|-Xaa. Leu-|-Xaa.
-!- TISSUE SPECIFICITY: Midgut.
-!- TESSUE SPECIFICITY: Midgut.
-!- DEVELOPMENTAL STAGE: Induced in the midgut of female after blood
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBL_TaxID=7165;
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InterPro; IPR001314; Peptidase_S1.
R InterPro; IPR001244; Peptidase_S1.
R InterPro; IPR001244; Peptidase_S1A.
R Ffam; PR00089; trypsin; 1.
R PRINTS; PR00722; CHYMCTRYPSIN.
R SMART; SM00020; Tryp_SPc; 1.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
R Hydrolase; Senies protease; Signal; Zymogen; Digestion; Multigene family.
R SIGNAL 17 POTENTIAL.
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                                                                                                                                                              Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases
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CHARGE RELAY SYSTEM
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    SIMILARITY: Belongs to peptidase family S1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                             SEQUENCE FROM N.A.
STRAIN-Suakoko, TISSUE-Midgut;
Mueller H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z18897, CAA79325.1; -.
EMBL; Z32645; CAA83568.1; -.
BYR; S49129; S49129.
HSSP; P00761; 1EPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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63 LLNDRWVL 70
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333 2
119 11
212 2
59 1
208 2
259 AA;
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es 6; Conserv
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SEQUENCE FROM N.A.
TISSUB-Venom gland;
MEDLINE-97056898; PubMed-8941719;
Deshinaru M., Ogawa T., Nakashima K., Nobuhisa I., Chijiwa T.,
Shimohigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S.
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
NCBI_TaxID=88087;
                                                                                                                                                                         "Accelerated evolution of crotalinae snake venom gland serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                           enzymatic activity.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICIAT: Expressed by the venom gland.
---- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                           Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Snake venom serine protease-like protein. Has lost two of the three essential catalytic residues and so probably has no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

VENOM SERINE PROTEINASE-LIKE PROTEIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINED (GLCNAC. . ) (POTENTIAL).

N-LINED (GLCNAC. . . ) (POTENTIAL).

N-LINED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                            SEQUENCE FROM N.A.
TSSUB-VENOR gland;
IN Q.M., Jin Y., Wei J.F., Wang W.Y., Xiong Y.L.;
"CDNA cloning of serine proteinases from the venom of Trimeresurus
            28-FEB-2003 (Rel. 41, Last annotation update)
Venom serine proceinase-like protein precursor (SP1).
Trimeresurus jerdonii.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eupldosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 260; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR009003, Cya_Ser_trypsin.
InterPro; IPR001054; Peptidase_S1.
InterPro; IPR01134; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPF; 1.
PROSITS; PS0240; TRYPSIN DOM; 1.
Serine procease homolog; Glycoprotein; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1692283141E12896 CRC64;
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'SP2 TRIFL

D VSP2 TRIFL

C 013057;

T 16-OCT-2001 (Rel. 40, Last sequence update)

T 28-FRB-2003 (Rel. 41, Last annotation update)

T 28-FRB-2003 (Rel. 41, Last annotation update)

We have a proteinase 2 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF292110; AAG10788.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 78.7%;
Similarity 75.0%;
6; Conservative
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260 AA;
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Best Local Similarity
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                  jerdonii.
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                                                                                                                                                                                                                                                                                                                                                                  DESTINATION SERIAL SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
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Pred. No. 7;
3; Mismatches 1; Indels
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable arginyl-tRNA--protein transferase (EC 2.3.2.8)
transferase) (Arginyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.7%;
55.6%;
                                                                                                                                 EMBL; D67079; BAA19977.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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260
1112
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1165
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55 ILINQEWUL 63
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260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
ATE PSEPK
ID ATE PSEPI
AC Q88FS6;
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TLF2. Trimeresurus flavoviridis (Habu). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.020; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
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ACT_SITE
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                                                                                                                    ESQUENCE FROM N.A.

**REQUENCE FROM N.A.*

**REQUENCE FROM N.A.*

**REQUENCE FROM N.A.*

**REQUENCE FROM N.A.*

**REQUENCE FROM N.B.*

**REQUENCE FROM N.B.*

**RETAINS dos Santos V.A.P.*, Fouts D.E., Gill S.R., Pop M., Holmes M.,

**Amartins dos Santos V.A.P.*, Fouts D.E., Gill S.R., Pop M., Holmes M.,

**Amartins dos Santos V.A.P.*, Fouts D.E., Kolonay J.,

**Reduence M.*, Mitte O., Peterson J., Khouri H., Hance I.,

**Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,

**Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,

**Auther J., Stippandic D., Hoheisel J., Straetz M., Heim S.,

**Auther J., Stippandic D., Hoheisel J., Straetz M., Heim S.,

**Akiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tummler B.,

**Riewitz C.,**

**Riewitz C.M.*

**Riewitz C.M.*

**Riewitz C.M.*

**Araser C.M.*
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                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M.;
"Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440.";
metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
-!- FUNCTION: Functions in the N-end rule pathway of protein
degradation where it conjugates Arg from its aminoacy1-tRNA to th
N-termini of proteins containing an N-terminal aspartate or
glutamate (Potential).
-!- CATALXTIC ACTIVITY: L-arginy1-tRNA + protein = tRNA + L-arginy1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UKRO, Q9UKRI;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Kallikrein 12 precursor (RC 3.4.21.-) (Kallikrein-like protein
                      Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AA; 27889 MW; F9C30B85BCDAE860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (Potential). SIMILARITY: Belongs to the R-transferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AA.
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MEDLINE=20118156; PubMed=10652563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016788; AAN69600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00689; -; 1.
InterPro; IPR007472; ATE C.
InterPro; IPR007471; ATE C.
Pfam; PF04377; ATE C.
Pfam; PF04376; ATE C.
1.
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225 LLINQRWV 232
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                                                                                                    NCBI_TaxID=160488
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KLK12 OR KLKL5.
PP4006
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Best Local S:
Matches 5
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g
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HUMAN
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-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Lawriter, Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Arallano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Yousef G.M., Luo L.-Y., Diamandis B.P.; "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4.";
                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;

Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.
Moss P., Paeper B., Wang K.; analysis of the serine protease gene
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolypsis and peptidolysis; NAS.
InterPro; IPRO01039; Cys Ser trypsin.
InterPro; IPRO01254; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
(BY
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM0020; TRYPSIN 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
HYDO13es; Section protease; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9UKR0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999).
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MIM; 605539; -.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                         SEQUENCE
ACT SITE
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
CARBOHYD
CARBOHYD
VARSPLIC
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||::|||| 50 VLIDHRWYL 58

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Gaps

Query Match

76.6%; Score 36; DB 1; Length 248;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels

sarch completed: March 1, 2004, 17:29:57
ob time : 7 secs

Human sec Human nov

Polypepti Human sec Novel hum Protein a Human pol Polypepti Human pol Rat GRIIO Human pro Rat CRIII Human pro Rat CRIII Human pro Polypepti Human pro Human pro Polypepti Human sec Novel human sec Novel human sec Human sec

Aaw89030
Abb51130
Abb51130
Abb5130
Abc0884
Abc0884
Abc0884
Abc0884
Abc0884
Adc0276
Abc0884
Adc0276
Abc0884
Adc0276
Abc088638
Abc088838
Abc0888383
Abc0888383
Abc08888

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ALIGNMENTS
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                                      ABB51130
ABO45387
ABO45387
AAO08397
AAO08397
ABC00864
ABC00966
ABB709096
AAB91080
AAB87732
             ADA11692
AAW89030
Query Match
 Aae08240 Human str
Abg3378 Novel hum
Ada05732 Human NOV
Aar6788 Human str
Aaw05383 Human str
Abb84406 Human SCC
Abb84406 Human SCC
Abb8740 Amino aci
Abu07471 Protein d
Abu7440 Protein d
Abu8740 Auman str
Adb80484 Ovarian c
Aab51358 Human gas
Aab6558 Human gas
Aab6358 Human gas
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Human liv
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H. pylori
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                                                                                            March 1, 2004, 17:16:55 ; Search time 45.5556 Seconds
    (without alignments)
    55.820 Million cell updates/sec
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Abb8421 Abb8421 Abb84406 H
Abb84406 H
Abu07440 B
Abu07441 Abu07441 Abu07440 Abb26441 Abb86441 Abb86481 Abb86481 Abb86481 Abb863578 Abb86358 Abb82382 Abb82
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Abg46617 B
Aaw98431 B
                                                                                                                                                                                                                                                                                  1586107
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                  otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    using sw model
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ABG2378
ADA05732
AAN65732
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ABB84421
ABB84421
ABB84421
ABB84401
ABB84401
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AAM37771
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ABG59233
ABG46617
AAW98431
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
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Match
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E08240 AAE08240 stan AAE08240,	
	. AA 0
AAE08240;	
DI UI-NOV-2001 (Ilrac encry) XX	
	Human stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).
XX KW Stratum corneum chymotryps	Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
antisens	nt hyperplasia.
XX Home canions	
PN W0200159158-A1.	
XX PD 16-AUG-2001.	
PF 07-FEB-2001; 2001WO-US003977.	77.
11-FEB-2000; 2000US-00502600	.00
AX PA (UYAR-) UNIV ARKANSAS.	
PI O'brien TJ;	
DR WPI; 2001-514676/56.	
	Diagnosing cancer comprises detecting stratum corneum chymotrypsin
PT enzyme.	
AAA Claim 25; Page 103; 127pp; English.	English.
_	The invention relates to diagnosing cancer especially ovarian cancer, by
	stratum corneum chymotrypsin enzyme (SCCE). Proteases are
CC considered to be an integr	ğ,
	ive of their presence or absence are useful for
	cancer. The method is useful for diagnosing cancer,
	perplasia. The SCCE oligonucleotide may be used
	to treat a cancer selected irom ovarian, breast, immy, colom, prostate and other cancers in which SCCR is overexpressed. The present sequence
XX SQ Sequence 9 AA;	

8

a

SULT 2

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                              numan; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                 ADA05736 standard; protein; 198 AA.
                                                                                                                                                                                                                                                                                                         Human NOV18c protein SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001, 2001US-0326483P.
05-OCT-2001, 2001US-0327435P.
05-OCT-2001, 2001US-0327917P.
09-OCT-2001, 2001US-0328029P.
09-OCT-2001, 2001US-0328049P.
09-OCT-2001, 2001US-0328849P.
12-OCT-2001, 2001US-0328849P.
15-OCT-2001, 2001US-0328849P.
16-OCT-2001, 2001US-0329414P.
17-OCT-2001, 2001US-0330142P.
22-OCT-2001, 2001US-0341058P.
24-OCT-2001, 2001US-0341058P.
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                                                                                                                                                                                                                                                              (first entry)
                                                                           12 LiPLOILL 20
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N-PSDB; ADA05735.
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16-MAY-2002; 2
16-MAY-2002; 2
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1-NOV-2001;
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                                                                                                                                                                                                                         ADA05736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollgomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, formalic for generatic disorders or other traits to assess biodiversity responsible for generatic disorders or other traits to assess biodiversity and to cid sequences. Abgonolo-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at (It) whip. int/pub/published_pot_sequences
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                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                       Indels
                 Pred. No. 1.4e+06; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #23369.
                                                                                                                                                                                                                           ABG23378 standard; protein; 136 AA.
30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.
9; Conservative
                                       9; Conservative
                                                                                  1 LLPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                 Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS87565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Local S:
Matches 9
                                                                                                                                                                                                                                                                   ABG23378;
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WO2003029424-A2

The present invention describes NOVX proteins, where X can be 1 to 55 cego. NOV1) Also described: (1) a composition comprising a polypeptide described above and a cartier; (2) a kit comprising, in one or more centainers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the business of the polypeptide described above; (5) a cell comprising the business of the polypeptide described above; (5) a cell compression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a pathology that is related to an aberrant expression of the above polypeptide or modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulation or compression of the polypeptide; (13) a method for modulation or preventing a pathology associated with the above polypeptide; uncorrective, antipacting or preventing a pathology associated with the above polypeptide; uncorrective, antipacting or protein and antilipacemic activities, and can be used in gene therapy. The polypeptide is useful in menufacturing a medicament; or prevent metabolic and molecule may be used to diagnose, treat or prevent metabolic activities, and can be used in gene therapy. The polypeptide is useful in menufacturing a medicament; or prevent metabolic activities, had menufolement and insorders and variance or obesity, infections, cancer, calculation and disorders become associated with a human disease. The polypeptide or prevent metabolic disorders under a plabetes or obesity, infections, cancer, in probes, in chromosome mapping New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Claim 1; Page 170; 586pp; English.

Sequence 198 AA;

Gaps ö 100.0%; Score 40; DB 6; Length 198; 100.0%; Pred. No. 14; 0; Indels Mismatches 0, Local Similarity 100 Query Match Best Loc Matches

Q 1 LIPLOILLL

ADA05732 standard; protein; 250 AA

(first entry) 06-NOV-2003

Human NOV18a protein SEQ ID NO:92.

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

Ношо

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05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328056P.
                                                                                                                                                                                                                                        18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
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2002US-0373815P.
2002US-0373817P.
2002US-0373864P.
2002US-0374977P.
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15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330142P.
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2002US-0381038P.
2002US-0381042P.
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2002US-0383656P.
2002US-0383831P.
02-OCT-2002; 2002WO-US031373
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19-APR-2002;
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(CURA-) CURAGEN CORP.

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36 N-PSDB; ADA05731.

ö

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing

obesity, or

Claim 1; Page 169-170; 586pp; English

pharmacogenomics

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the mucleic acid molecule described above; (5) a cell
comprising the polypeptide described above; (5) a cell
prise to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
copypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
the intracting a pathology that is related to an aberrant expression or
aberrant physiclogical interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to

Sequence 253 AA;

field.)

SXS

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a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide. Norward and (14) a method for producing the above polypeptide. Norward sequences have antidabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, noorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a polypeptide is useful, in manufacturing a medicament for treating a acid molecule may be used to diagnose, treat or prevent metabolic alsorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders used as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
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Sequence 250 AA;

ö Gaps ; 0 100.0%; Score 40; DB 6; Length 250; 100.0%; Pred. No. 18; 0; Indels 0; Mismatches Conservative 1 LLPLQILLL 9 Local Similarity les 9, Conserv Query Match Matches

Libroitit 11

AAR67888 standard; protein; 253 AA ESULT 5 AR67888

(revised)
(first entry) 25-MAR-2003 AAR67888;

09-AUG-1995

Human stratum corneum chymotrophic recombinant enzyme (SCCE).

Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.

Homo sapiens

WO9500651-A1

94WO-IB000166 20-JUN-1994;

05-JAN-1995.

93DK-00000725 18-JUN-1993;

(SYMB-) SYMBICOM AB

Egelrud T, Hansson L;

WPI; 1995-052088/07.

N-PSDB; AAQ81203

Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.

Disclosure, Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p5507. (Updated on 25-MAR-2003 to correct PN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cpds. useful for treating or produces for the design associated with beta-amyloid peptide, esp. Alzeimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                           Gaps
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100.0%; Score 40; DB 2;
100.0%; Pred. No. 18;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                         Human amyloid precursor protein protease.
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ABB84421
ID ABB84421 standard; peptide; 253 AA.
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                                                                                                                                            AAW05383 standard; protein; 253 AA
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 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAT39783.
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                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                       AAW05383;
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Best Local
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                                                                                                                   RESULT 6
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ABB84421;
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08-NOV-2002 (first entry)

Human SCCE protein N-terminal fragment SEQ ID 48.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens

WO200262135-A2.

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-0000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

Egelrud T, Hansson L;

WPI; 2002-643380/69

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Example 6; Page 37; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a mucleotide sequence coding for a stratum corneuw chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal compounds at opic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal compounds with human variation compound conteum corneum fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the transgenic mammals described in the invention

Sequence 253 AA;

Gaps . 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; cive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

LEPLOILL 14 9

1 LLPLQILLL 9

ABB84406 standard; protein; 253 AA.

ABB84406;

(first entry) 08-NOV-2002

Human SCCE protein.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; kran eancer; hyperkersetosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens

15-AUG-2002.

WO200262135-A2.

08-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

ï Egelrud T, Hansson

WPI; 2002-643380/69. N-PSDB; ABQ76226.

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide endrowed at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be useful for screening or identifying a compound or composition effective for the prevention or identifying a compound or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal contrus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful contraction or for further studies of itch mechanisms and the testing of epidermal and now more and inherited skin diseases and inherited skin diseases and now more and inherited skin diseases and now more and inherited skin diseases and now more and the testing of epidermal and more and inherited skin diseases and now more and inherited skin diseases and inherited skin diseases and inherited skin diseases and inherited skin diseases and inhe potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotraptic enzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (KLK7) and is used in the development of the transgenic mammals described in the invention

Sequence 253 AA;

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0; Gaps 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

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ESULT 8 BB84406

AAU82740 standard; protein; 253 AA

(first entry) 23-APR-2002 Amino acid sequence of novel human protease #39.

Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease, metabolic disorder; inclammatory disorder; nervous system disorder, sexual dysfunction, pain; mood disorder, hypertension, psychocic disorder; neurological disorder, dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme

Homo sapiens.

WO200200860-A2.

03-JAN-2002

26-JUN-2001; 2001WO-US020171

26-JUN-2000; 2000US-0214047P

(SUGE-) SUGEN INC.

Sudarsanam S, Manning G, Caenepeel S; Whyte D, Plowman G,

WPI; 2002-139913/18.

Charydczak G;

N-PSDB; ABK31782

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders.

Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and astima), cardiovascular diseases (e.g. inflammatory diseases, metabolis, brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. disorders, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheiner's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also virus (HIV), and non-viral infections caused by human immunodeficiency glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention

Sequence 253 AA;

Gaps 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; 0; Indels 0; Mismatches Conservative Query Match Best Local Similarity Matches 9; Conserv

LLPLOILLL 14 σ 1 LLPLQILLL

ABU07440 standard; protein; 253 AA. 

ABU07440;

28-JAN-2003

Protein differentially regulated in prostate cancer #43.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.

Homo sapiens.

WO200281638-A2.

17-0CT-2002.

08-APR-2002; 2002WO-US010824,

06-APR-2001; 2001US-0281731P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z,

WPI; 2003-058520/05. N-PSDB; ABX10343 Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of the probability that the sample comprises the number of the probability that the sample comprises the number is indicative of the probability that the sample comprises or the number is indicative of the probability that the sample comprises or prevention in a subject having a prostate cancer. Which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) to useful as molecular markers, as drug targets, and for detecting, or useful as molecular markers, as drug targets, and for detecting, or products are used in the diagnostic test to assay for presence of cancer. (I) is useful and the diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. (I) is useful for assessing cancer e.g., to determine the type of earching specific binding partners of the polypeptide and thus of specific genes, and groups of genes a target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus of specific genes, and groups of genes, expressed in pathways of the polypeptide and in the diagnostic prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and croup of genes of a p regulated in prostate cancer

AA; Sequence 253

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Gaps

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Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer, gene expression, differential regulation, molecular marker, drug target, cancer detection, cancer diagnosis, cancer staging, cancer grading, cancer assessing, cancer monitoring
                Length 253;
                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Protein differentially regulated in prostate cancer #74.
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                Score 40;
Pred. No. 1
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                  100.0%;
100.0%;
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Query Match
Best Local Similarity 100.
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises for prostate cancer. (I) Is useful for assessing a therapeutic or prevention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of trayet genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate tissue (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells, which a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as markers, as drug targets, and for detecting. diagnosing, stading, grading, gasessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus

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Gaps

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Indels

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core 40; DB 6 red. No. 18; Mismatches

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RESULT 13

Score 40; Pred. No.

100.0%;

Query Match Best Local Similarity

Best Loc Matches

Length 253,

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for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of bunctional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially regulated in prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         ABR58471 standard; protein; 253 AA.
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                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
and as vaccines. This sequence corresponds to one of the proteins used
for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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                                                                                                                                      cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
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larity 100.0%; Pred. No. 18;
Conservative 0; Mismatches 0; Indels
                                                                                                              Ovarian cancer-associated protein #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB21326 standard; protein; 257 AA.
                 ADB80484 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 291; 332pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                   27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-0317544P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                        18-JUN-2002; 2002WO-US019297
                                                                                                                                                                                                                                                                                                                                       2001US-0299234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-167431/16.
N-PSDB; ADB80483.
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gish KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 253 AA;
                                                                                                                                                                                                                                          WO2002102235-A2
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                       18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2001
                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                           27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB21326;
                                                ADB80484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESULT 14
 DB80484
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The present sequence is human stratum corneum chymotryptic enzyne (HSCEB), a member of the kallikrein multi-gene family. Kallikreins and kallikrein-like proteins are a subgroup of the serine proteins enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic cids encoding kallikrein-like proteins KKL*Li, KKK-Li, KKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gastric cancer associated antigen protein sequence SEQ ID NO:942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                             Human, KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6; HSCEE;
human stratum corneum chymotryptic enzyme; kallikrein-like protein;
serine protease; cytostatic; cancer; prostrate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, breast cancer, gastric cancer, prostate cancer, diagnosis; cancer associated antigen, cytostatic, cancer vaccine.
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99US-0127386P.
99US-0144919P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200073801-A2.
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999;
21-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L4-SEP-2000.
Human HSCEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB63580;
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(LUDW-) LUDWIG INST CANCER RES
                                                                                                             WPI; 2001-025274/03.
28-MAY-1999;
10-SEP-1999;
                                                                              Obata Y;
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99US-0136526P. 99US-0153454P.

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 prepresent nucleotide sequences encoding human breast, gatarric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein, e.g. cancer
Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g. cancer.
                                                                                                                                                                                                                                                                                    Example 1; Page 625; 799pp; English.
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Sequence 142 AA;

0; Gaps Query Match 95.0%; Score 38; DB 4; Length 142; Best Local Similarity 88.9%; Pred. No. 23; Matches 8; Conservative 1; Mismatches 0; Indels

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earch completed: March 1, 2004, 17:28:52 ob time: 46.5556 secs

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Sequence 2, Appli
Sequence 3, Appli
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Sequence 13, Appli
Sequence 1033, Appli
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Sequence 1079, A
Sequence 22870,
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                                                                    March 1, 2004, 17:21:46; Search time 11.8889 Seconds (without alignments) 39.081 Million cell updates/sec
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Sequence 3
Sequence 3
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-918-243-35
US-08-918-24-44-2
US-08-9154-344-2
US-08-910-184-3
US-09-154-344-2
US-09-910-184-3
US-09-764-76-3
US-09-764-76-3
US-09-918-24-3
US-09-918-24-3
US-09-918-24-3
US-09-918-24-3
US-09-918-24-3
US-09-393-634-3
US-09-48-0334-12075
US-09-48-0334-12075
US-08-339-152A-17
US-08-339-152A-17
US-08-339-152A-17
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US-09-245-041-15
US-09-502-600-36
US-09-918-243-36
                                                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                              ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Match Length DB
                                                                                                                                               1 LLPLQILLL 9
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100.0
100.0
90.0
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TYPE: PRT ORGANISM: Homo sapiens

LENGIH: 9

US-09-502-600-35

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

Parent No. 6294344

TYLLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: US/09/502,600A

TITLE APPLICATION NUMBER: US/09/502,600A

PRIOR FILING DATE: 09/039,211

PRIOR FILING DATE: 09/039,211

NUMBER: OF SEQ ID NOS: 136

LENGTH: 9 ö 20, Appli 20, Appli 20, Appli 20, Appli 20, Appli 40, Appli 40, Appli 40, Appli 40, Appli 5063, Appli US-09-918-243-35

Sequence 35, Application US/09918243

Sequence 35, Application US/09918243

Sequence 35, Application US/09918243

Sequence 35, Application GE242019

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6232(IP/C/D/CIP)

CURRENT APPLICATION NUMBER: US, 09/9918,243

CURRENT FILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35 Gaps sednence sed Sequence Sequence Sequence Sequence Sequence ö 100.0%; Score 40; DB 3; Length 9; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-28 US-08-713-556-42 US-08-713-556-36 US-08-713-556-36 US-08-713-556-36 US-08-713-556-36 US-08-713-556-2 US-08-477-254A-2 US-08-477-254A-2 US-08-713-556-2 US-08-713-556-2 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-08-713-556-4 US-09-134-001C-5063 US-09-134-001C-5063 ALIGNMENTS Query Match
Best Local Similarity 100.
Matches 9; Conservative TYPE: PRT ORGANISM: Homo sapiens FEATURE: σ US-09-502-600-35 Н RESULT 2 ઠ 셤

us-09-905-083-35.rai

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US-08-824-874-3
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Sequence 2. Application US/08557146
Sequence 2. Application US/08557146
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beglind, Torbjorn
APPLICANT: Beglind, Tennart
TITLE OF INVENTION: Enarge (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: New York
COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: WAS A 24
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 1103326-181
TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 253;
                                                                                             100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
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NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
3-09-918-243-35
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0; Mismatches
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Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOLECUT 253 amino acids
TYPE: amino acids
TOPOLOGY: 11-
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
S-08-557-146-2
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                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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Gaps
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| Sequence 2, Application US/09154344
| Patent No. 5891256
| GENERAL INFORMATION:
| APPLICANT: Bealson, Lemnart
| TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
| TITLE OF INVENTION: Enzyme (SCCE)
| TITLE OF INVENTION: Enzyme (SCCE)
| TITLE OF INVENTION: Enzyme (SCCE)
| TORRESPONDENCE ADDRESS:
| CORRESPONDENCE ADDRESS:
| STREET: New York STREET: New York STRIE: TORSON STRIE: New York STRIE: New York STRIE: TORSON STRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2; Length 253;
Pred. No. 3;
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                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                     Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 омвЕR: US/09/154,344
16-SEP-1998
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NAME: Billings, Lucy J.
REGISTRATION INVHRER: 36,749
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEFRAN: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                              SEE: Incyte Pharmac.: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pi
STREET: 3174 Porter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: GenB
CLONE: 532504
                                                                                                                                                                                USA
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                                                                                                                                                                                                       94304
                                                                                                 CITY: Pa.
STATE: CA
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us-09-905-083-35.rai

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100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 3;
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3;
                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUT TYPE: Disketter
COMPUTER: IBM Compacible
OPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
SOFTWARE: FASTERGE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BILINGS, LUCY
REGREENCE/DOCKET NUMBER: 36,749
REGREENCE /DOCKET /DOCKET /DOCKET /DOCKET /DOCKET /DOCKET /DOCKET /DOCKET /DOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUTRY: USA
ZIP.
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Lal, Preeti
LILE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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105-09-764-762
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Patent No. 6197511
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 9; Conservative
                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
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US-09-210-084-3
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Sequence 2. Application US/08930188

Patent No. 6093397

GENERAL INFORMATION:

APPLICANT: Dixton, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3
CORRESPONDENCE BILLILILY and Company
STREET: Lilly Corporate Center
CITY: Indiana
CONTRY: United States of America
ZIP: Ad6285.
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
CITY: Indiana
CONTRY: United States of America
ZIP: A6285.
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE:
CREENT APPLICATION DATA:
CREENT APPLICATIO
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Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REPERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 819-8783
TELEFAX: (212) 819-8783
TELEFAX: (212) 344-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: proctein
S-09-154-344-2
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CLASSIFICATION:
PLOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 04-APR-1955
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERRNCE/DOCKET NUMBER: X9239
TELECHONE: 317-277-1090
TELECHONE: 317-277-1090
TELEFAX: 317-277-1090
TELEFAX: 317-277-1090
TELEFAX: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: slingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein IS-08-930-188-2
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Gaps
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Gaps

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Patent No. 629434

Patent No. 629434

GENERAL INFORMATION:

TILLE OF INVENTION:

TILLE OF INVENTION:

TILLE REPRENCE:

FILE REPRENCE:

CURRENT FILING DATE: 2000-02-11

CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR APPLICATION NUMBER: US/09/502,11

PRIOR PRIOR OF EQ ID NOS: 136

SEQ ID NOS: 136

LENGTH: 9

LENGTH: 9

LENGTH: 9
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Patent No. 6627403

RAPELICANT: O'BRIEN, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
IITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REPERENCE: D6220IP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels
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, OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTAATION NUMBER: X9239
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
TELEPAX: 317-277-361
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PRIOR FILING DATE: 2001-07-13
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US96-04294-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF SEQUENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                 STREET: 31/4 FORCET DILIVE
CUITY: Palo Alto
STARTE: CA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: ISM Compatible
CORPUTER: ISM COMPATA: US/09/764,762
FILLING DATE: 16-Jan-2001
CLASSIFICATION NUMBER: US/09/764,762
FILLING DATE: 16-Jan-2001
CLASSIFICATION NUMBER: 09/210,084
FILLING DATE: -UNKNOWN-
ATTOREY/AGENT INFORMATION:
NAMME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELEROMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:

ZIP: 46285

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

OPERATING SYSTEM: PC-DOS/NS-DOS

OPERATING SYSTEM: PC-DOS/NS-DOS

OPERATING SYSTEM: PAC-DOS/NS-DOS

OPERATING 
                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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100.0%; Score 40; DB
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
S-09-764-762-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Bli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LiPLOILL 14
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NAME/KEY: SITE
CCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-03-205-258-1083
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Separation
APPLICANT: Adler, Separation
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.0%; Score 34; DB 4; Length 73; 87.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                   EARLIER FILLING DATE: 1997-06-06
EARLIER PELLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-07-05-06
EARLIER FILLING DATE: 1998-07-130
NUMBER OF SEQ ID NOS: 1227
ESQ ID NO 1083
LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/09393634 Patent No. 6558910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 36; DB 4; Length 9; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
S-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEREAL NO. 65.21/4

APPLICANT: Young et al.

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPERNCE: PZ607P1

CURRENT PILING DATE: 1998-10-04

EARLIER APPLICATION NUMBER: BC7/US98/11422

EARLIER PILING DATE: 1998-6-04

EARLIER PILING DATE: 1998-06-04

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997
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APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1083, Application US/09205258
Patent No. 6525174
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLPLQILL 9
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S-09-205-258-1083
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Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Young et al.

FILLE REPERENCE: POOD PU

CURRENT APPLICATION NUMBER: US/09/205,258

EARLIER APPLICATION NUMBER: US/09/205,258

EARLIER FILING DATE: 1998-06-04

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1997-06-05

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-05

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,892

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,893

EARLIER FILING DATE: 1997-06-06

EARLIER F
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 37
LENGTH: 302
                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GR02
NAME/KEY: MOD RES
LOCATION: (143)
OTHER INFORMATION: Xaa = any amino acid
S-09-393-634-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 14
S-09-205-258-1079
Sequence 1079, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
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TYPE: PRT
PGRANISM: Homo sapiens
PERTURE:
NAME/KEY: SITE
COCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (359)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1079
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LOCATION: (314)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
PEATURE:
LOCATION: (359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.0%; Score 34; DB 4; Length 424; Best Local Similarity 87.5%; Pred. No. 70; Matches 7; Conservative 1; Mismatches 0; Indels
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1998-07-30
SEQUIDADE: 10099-07-30
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US-09-252-991A-22870
; Sequence 22870, Application US/09252991A
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us-09-905-083-35.rai
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Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC AID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13 6
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Pred. No. 95;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
3-09-252-991A;22870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.0%;
Best Local Similarity 77.8%;
Matches 7; Conservative 1
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1 LLPLQILLL 9 |||| :||| 51 LLPLSVLLL 59

aarch completed: March 1, 2004, 17:38:24
3b time : 11.8889 secs

Seguence 2472, Ap

Sequence 37, Applia Sequence 37, Applia Sequence 1079, Applia Sequence 1079, Applia Sequence 1079, Applia Sequence 20447, A Sequence 20447, A Sequence 99, Applia Sequ

Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

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US-09-16-243-35

US-09-16-243-35

Sequence 35, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6223CIP/C/D/CIP

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CHAIN
; CTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35
5 US-10-264-237-2472

0 US-09-956-632A-39

0 US-09-9510-332-37

0 US-09-9510-332-37

4 US-10-383-982-37

4 US-10-383-982-1079

4 US-10-023-282-1079

4 US-10-023-282-1079

4 US-10-023-282-1079

5 US-10-291-265-409

1 US-09-989-72-99

1 US-09-989-72-99

1 US-09-989-73-99

1 US-09-989-73-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-905-083-35
Sequence 35, Application US/09905083
Patent No. US20020146708A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LLPLOILLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                   March 1, 2004, 17:35:01 ; Search time 24.1111 Seconds (without alignments) 78.818 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. (cgn2_6/ptodata/1/pubpa/USO7_PUBCOMB.pep:*
2. (cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/PCTUB/PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
4. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
5. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
6. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-083-35
US-09-888-615-98
US-09-764-762-3
4 US-10-264-283-90
5 US-10-295-027-498
5 US-09-918-243-33
US-09-905-083-33
US-09-905-083-33
US-09-864-761-6097
US-09-864-761-6097
US-09-865-913A-92
4 US-10-097-065-220
4 US-09-33-3767-1083
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                                                                                                                                                                                                                                                                                                                                                                                809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             inimum DB seq length: 0 aximum DB seq length: 200000000
                                                                                                                                                                                                                                   US-09-905-083-35
40
1 LLPLQILLL 9
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Match Length DB
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                                                                                                                                                                                                                                                                                                                      coring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atabase :
                                                                                                                                                                                                                                                                                 equence:
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                                                                                                                                                          <u>..</u>
                                                                                                                                                                                                                                     itle:
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No.
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Gaps

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Length 9;

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CITY: Palo Alto
                                               USA
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CRGANISM: Homo sapiens
US-10-264-283-90
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US-10-264-283-90
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FITLE OF INVENTION: Ovarian Cancer
FITLE REPERBNCE: D622301P/C/D10
CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
SEQ ID NO 35
LENGTH: 9
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100.0%; Score 40; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                       NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
3-09-905-083-35
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 9; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09764762
Patent No. US20020068341A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TILLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PLOWARN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CARNEREL, SEAN
APPLICANT: CARNEREL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TILLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98, Application US/0988615
Patent No. US20020064856A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
S-09-888-615-98
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
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LLPLQILLL 14
                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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3-09-888-615-98
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 9; Length 253; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Algate, Paul A. APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane APPLICANT: Mannion, Jane APPLICANT: Mannion, Jane TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REPERENCE: 2.1012.1.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT PLING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: COTIXA INVENTION DISCIOSURE DATABASE
SEQ ID NO 90
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                         CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/210,084
FILING DATE: CUNKNOM:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10264283; Publication No. US20030144494A1; GENERAL INFORMATION:
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                          OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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Query Match
Best Local Similarity
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US-09-905-083-33
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                                                                                                                                                  APPLICANT: ALEX, Natasha
APPLICANT: ALEX, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Richard
APPLICANT: Given, Richard
APPLICANT: Marcy Richard
APPLICANTON: Methods of Enseming for Modulators of Cancer
FILE REPERSINCE: 018 500-11-30 80/663,733
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/345,314
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR PILING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR PILING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR APPLICATION NUMBER: US 60/355,7250
PRIOR APPLICATION NUMBER: US 60/355,72
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Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions TITLE OF INVENTION: Methods of Screening for Modulators of Ovarian TITLE OF INVENTION: Cancer FILE REFERENCE: 018501-002420US
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                     Sequence 498 Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
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10-295-027-498
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US-09-918-243-33

US-09-918-243-33

Sequence 3.3 Application US/09918243

Sequence 3.3 Application US/020142317A1

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION Methods for the early diagnosis of ovarian cancer;
TILE REFERENCE: D6223GTP/C/D/1918,243

CURRENT APPLICATION NUMBER: US/09/918,243

FRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 136

LENGTH: 9
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Patent No. US20020146708A1

Patent No. US20020146708A1

Patent No. US20020146708A1

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian cancer FILE REPERBURE: D62230IF/C/Day

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT APPLICATION NUMBER: US/09/905,083

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2000-02-11

SEQ ID NO 33

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-08-27
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 48
LENGTH: 253
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Gaps
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             PRIOR APPLICATION NUMBER: PCT/USOL/OGG9
PRIOR APPLICATION NUMBER: PCT/USOL/OGG9
PRIOR APPLICATION NUMBER: PCT/USOL/OGG9
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USOL/OGG6
PRIOR APPLICATION NUMBER: PCT/USOL/OGG6
PRIOR FILING DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-20
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DAT
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Pred. No. 12;
2; Mismatches 0; Indels
PCT/US01/00666
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Best Local Similarity 77.8
Matches 7; Conservative
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US-09-895-913A-92
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Sequence '46097, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION UNMER: US/09/864,761
CURRENT FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-06-06
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Walry S.
APPLICANT: Glodman, Walleng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5.05.2) B
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10.255
LENGTH 868
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Pred. No. 3.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                              Query Match

90.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAMPÍXEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
S-09-905-083-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10255, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Cytophaga hutchinsonii IS-10-369-493-10255
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                          87.5%; Score 35; DB 9; Length 480;
88.9%; Pred. No. 2.6e+02;
vative 0; Mismatches 1; Indels
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GENERAL INFORMATION:

TITLE OF INVENTION: 110 Human Secreted Proteins
FILLE REFERENCE: P2021P1
CURRENT APPLICATION NUMBER: US/10/097,065
CURRENT FILING DATE: 2002-03-14
PRIOR FILING DATE: 1998-12-17
PRIOR FILING DATE: 1998-12-17
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR PELICATION NUMBER: 60/068,057
PRIOR FILING DATE: 1997-12-18
PRIOR PELICATION NUMBER: 60/068,369
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
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... OTHER INFORMATION: Xaa equals stop translation US-10-097-065-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 220, Application US/10097065
Publication No. US20030055236Al
GENERAL INFORMATION:
ORGANISM: Helicobacter pylori
S-09-895-913A-92
                                                                                                                  Query Match
Best Local Similarity 88.9°
Matches 8; Conservative
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8 8

RESULT 14 US-09-933-767-1083

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CURKERY FILING DATE: 2011.12.20
CURKERY FILING DATE: 1936-12-14
ERALIER PILING DATE: 1936-16-06
ERALIER PILING DATE: 1936-06-06
ERALIER PILING DATE: 1936-06-06
ERALIER PILING DATE: 1937-06-06
ERALIER PILING DATE: 1937-06-0
                                               APPLICATION NUMBER: US/10/023,282
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LOCATION: (8)
CTHEN INFORMATION: Xaa equals any of the naturally occurring L-amino acids
S-09-933-767-1083
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85.0%; Score 34; DB 10; Length 73;
Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 0; Indels
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Sequence 1083, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
IITLE OF INVENTION: 207 Human Secreted Proteins
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1998-01-30
PRIOR PELING DATE: 1998-05-18
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ORGANISM: Homo sapiens
FEATURE:
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S-10-023-282-1083
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EARLIER APPLICATION NUMBER: 60/048,963

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER PILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-12-18

BARLIER FILING DATE: 1997-12-19

BARLIER FILING DATE: 1998-07-15

BARLIER APPLICATION NUMBER: 60/094,657

BARLIER FILING DATE: 1998-07-15

BARLIER PILING DATE: 1998-07-15

BARLIER PILING DATE: 1998-07-15

BARLIER FILING DATE: 1998-07-15

BARLIER APPLICATION NUMBER: 60/094,657

BARLIER FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PATEMENT OF SEQ ID NOS: 1227

SEQ ID NO 1083

LENGTH: 73

TYPE: PRT

ORGANISM: Home sapiens

FEATURE:

NAME/KER:

NAM
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earch completed: March 1, 2004, 18:08:51 ob time : 25.1111 secs

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                                          March 1, 2004, 17:21:01; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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T29010 A31759	S23756 A83214 T43766	G65039 A54984	JE0322 C84914	H86811 A41720	A41927 AB3334	A98157 AH3130	T26360
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## ALIGNMENTS

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RESULT

A;Cross-references: GB:AE001437; PIDN:AAK80095.1; PID:g15025128; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics: A;Gene: CAC2137

90.0%;

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

670 LLPIQILLI 678

1 LLPLQILLL 9

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heretocarcinogenesis-related transcription factor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Ciscession: UC4857
Rickensesion: UC4857
Rickishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Rickishimoto, T.; Kokura, Commun. 224, 746-751, 1996
A.Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB:
A;Reference number: UC4857
A;Accession: UC4857
A;Molecule type: mRNA
A;Residues: 1-267 <KIS>
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: 833603
A;Lim, B.L.; Lu, V.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot A;Reference number: 833603; MUID:93170856; PMID:8436402
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: JC7300 B;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K. D. Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K. J. 197-193, 2000 A;Atitle: Isolation and characterization of the gene encoding mouse tax-responsive element A;Reference number: JC7300 A;Accession: JC7300 A;Accession: JC7300 A;Accession: JC7300 A;Accession: JC7300 A;Accession: JC56 AMS> A;Accession: JC56 AMS
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F;89-126/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: trebs
C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-369 <LIM>
C.Superfamily: pulmonary surfactant protein D, C-type lectin homology
F,248-367/Domain: C-type lectin homology <LCH>
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Pred. No. 30;
0; Mismatches
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Pred. No.
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88.9%;
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ilarity 88.9%;
Conservative
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JC4857
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; Tomb, J. R.; Wilte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne on, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. ature 388, 539-547, 1997

Atuthors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     onserved hypothetical integral membrane protein HP0946 - Helicobacter pylori (strain 26;Species: Helicobacter pylori
;Species: Helicobacter pylori
;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA; Molecule type: DNA; TOPA; Status (1496 < TOM) Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pothetical protein jhp0880 - Helicobacter pylori (strain J99)
Species: Helicobacter pylori
Variety: strain J99
Variety: strain J99
Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
Accession: A71875
Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Iture, C.7, Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; ture 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Genomic sequence comparison of two unrelated isolates of the human gastric path Reference number: A71800; MUID:99120557; PMID:9923682 Accession: A71875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
|Residues: 1-493 <ARN>
|Cross-references: GB:AE001518; GB:AE001439; NID:g4155454; PIDN:AAD06464.1; PID:g415546
|Bayerimental source: strain J99
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                                                       Score 36; DB 2; Length 845;
Pred. No. 39;
2; Mismatches 0; Indels
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Score 35; DB 2; Pred. No. 36; 0; Mismatches

87.5%;

Query Match 87.5 Best Local Similarity 88.9 Matches 8; Conservative

Gene: jhp0880

Status: preliminary

Libisitii 262

1 LLPLQILLL 9

- mouse

ax-responsive element-binding protein 5; Species: Mus musculus (house mouse)

ESULT 5 C7300

Conservative

Query Match Best Local Similarity Matches 8; Conserv

Start codon: GTG

|||| |||| 254 LLPLSILL 262

1 LLPLQILLL 9

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conglutinin - bowine
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus
C; Species: Bos primigenius
C; Species: Boser, Sp. 8.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, Gene 141, 27-281, 1994
R; Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, Gene 141, 1994
A; Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of A; Reference number: 145878; MUID:94215917; PMID:8163202
A; Recession: 145878
A; Molecule type: mRNA
A; Residues: 1-371 < LIO>
A; Molecule type: mRNA
A; Residues: 1-371 < LIO>
A; Cross-references: GB:L18871; NID:9495012; PIDN:AMAZ0126.1; PID:9495013
C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
F; 248-369/Domain: C-type lectin homology < LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Tutrons: 67/1; 106/1; 142/1; 178/1; 245/1

C; Superfamily: pulmonary surfactant protein D; C-type lectin homology

C; Superfamily: pulmonary surfactant protein D; C-type lectin homology

C; Superfamily: pulmonary surfactant protein D; C-type lectin homology

C; Reywords: calcium binding; glycoprotein; hydroxyproline

F; 1-20/Domain: signal sequence #status predicted <NAT>

F; 21-371/Product: conglutinin #status predicted <MAT>

F; 6-214/Region: collagan-like

F; 6-314/Region: collagan-like

F; 6-314/Region: C-type lectin homology <LCH>

F; 6-317/Product: conglutinin-N #status predicted <MAZ>

F; 6-318/Product: conglutinin-N #status gite: carbohydrate (Lys) (covalent) #status experimer

F; 63, 87, 99, 135, 141, 159, 162, 198, 210/Modified site: 5-hydroxylysine (Lys) #status experimer

F; 78, 96, 108, 111, 129, 132, 147, 153, 171, 195/Modified site: 4-hydroxyproline (Pro) #status experimental
     R.Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, J. Immunol. 153, 173-180, 1994
A;Tille: Bovine conglutinin gene exon structure reveals its evolutionary relationship to A;Accession: 146010; WJD:94267222; PMID:8207234
A;Accession: 146010
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Redecule type: DNA
A;Redecule type: DNA
A;Redecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PID:9514256; Comment: This protein mediates the agglutination of erythrocytes with antibody and comp. Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine.
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T17215
T17215
T17215
C1515
T17215
C2)Species: Homo sapiens (man)
C2)Species: Homo sapiens (man)
C2)Species: Homo sapiens (man)
C2)Species: Homo sapiens
C3)Species: Homo sapiens
C4)Species: Homo sapiens
C5)Species: Homo sapiens
C5)Species: Homo sapiens
C7)Species: Homo sapiens
C7)Species: T17215
C7)Species:
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Pred. No. 42;
1; Mismatches 1; Indels
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Pred. No. 42;
1; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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77.8%;
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es 7; Conserv
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A; Contents: annotation
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;Residues: 21-209, S',211-371 <LEE>
;Residues: 21-209, S',211-371 <LEE>
;Rawasaki, N.; Yokota, Y.; Kawasaki, T.
rch. Biochem. Biochem. 333-540, 1993
rch. Biochem. Biophys. 305, 333-540, 1993
;Reference number: S16879; MUID:93384312; PMID:8373191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA

*Residues: 1-371 <KAZA

*Residues: 1-371 <KAZA

*Note: The authors translated the codon GAT for residues 250 and 270 as Glu

*Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.

*Iochem. J. 292, 157-162, 1993

*Title: The CDNA cloning of conglutinin and identification of liver as a primary site

*Reference number: $33235; MUID:93277452; PMID:7684896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin Reference number: A23740; MUID:91131556; PMID:1993651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Bos prinigenius taurus (cattle)
Date: 10-Sep-1999 #text change 16-Jun-2000
Accession: JN0450; JC2396; S33235; A33740; S36879; S35044; I46010; A29416; S34054
Suzuki, Y.; Yin, Y.p.; Makino, M.; Kurimura, T.; Wakamiya, N.
Ochem. Biophys. Res. Commun. 191, 335-342, 1993
Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
Reference number: JN0450; MUID:93213261; PMID:8460993
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Residues: 21-54;75-86,'X',88-89,'X',91,'X',93-94;208-209,'X',211-227 <KAW>
Experimental source: serum
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Residues: 1-172, 'H',114-217,'A',219-271,'V',273-371 <LUU>
Cross-references: EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: DDBJ:D14085; NID:g285643; PIDN:BAA03170.1; PID:g285644
           Gaps
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Basidues: 75-86, X', 88-89, X', 91,'I' <LUA>
Basidues: 77-86, X', 88-89, X', 91,'I' <LUA>
Basidues: 78-86, X', 88-89, X', 91,'I' <LUA>
Basidues: 78-86, X', 88-89, X', 91,'I' <LUA>
Recommental source: Lung
Young, N.M.; Leon, M.A.
Young, N.M.; Leon, M.A.
Young, N.M.; Leon, M.A.
Young, N.M.; Leon, M.M.
Young, M.
Young, M.M.
Young, 
           Indels
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           ä
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: C3b-binding protein Contains: conglutinin-N
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                Conservative
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Residues: 1-371 <SUZ>
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                      Matches
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C;Accession: H84314
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Kaller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lis. A;Atterie: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
                                                                                                                                                                                         C)Accession: T50904

R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt;

A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt;

A;Accession: T50904

A;Accession: T50904

A;Accession: T50904

A;Resiues: 1-1236 «NAG»

A;Resiues: 1-1236 «NAG»

A;Coss-references: EMBL:AB034704; PIDN:BAA94057.1

A;Experimental source: Strain IL144

C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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C.Species: Halobacterium sp. NRC-1
C.bree: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Pyrococcus abyssi
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
CiAccession: H75201
                                                                                                                           C.Species: Rubrivivax gelatinosus
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
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LLPLQIIIV 76
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Matches 6; Conserv
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ses 8; Conserv
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Residues: 1-146 <KAW>
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A;Gene: PAB0088
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Matches
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Secondary, C.K.; Prwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
Secondary, C.K.; Pham, X.C.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Lim,
Jimon, S.; Vian, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Tature 406, 959-964, 2004
Tature 406, 959-964, 2004
Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,Status: preliminary
,Molecule type: DNA
,,Molecule type: DNA
,,Residus: 1-539 <RTO
,,Cross-references: GB:AE004934, GB:AE004091, NID:g9951515, PIDN:AAG08601.1; GSPDB:GN001
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Signeties: Homo sapiens (man)
Signeties: Homo sapiens (man)
Signete: 23-401-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
Signete: 23-401-1999 #sequence_revision 23-Jul-1999
Riwambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Pred. No. 62;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                         Length 429
                                Molecule type: mRNA
|Residues: 1-429 <POU>
|Cross-references: EMBL:AL117404
|Cross-references: EMBL:AL117404
|Cross-reference: adult testis; clone DKFZp434H2235
|Genetics:
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A, Experimental source: adult testis; clone DKFZp434G173
                                                                                                                                                                                                                                   Score 34; DB 2;
Pred. No. 49;
1; Mismatches
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Best Local Similarity 87.5
Matches 7; Conservative
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A;Molecule type: mRNA
A;Residues: 1-1092 <WAM>
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Status: preliminary
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1;Gene: PA5216

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Wed Mar 3 07:49:14 2004
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/Accession: H84314
/Status: preliminary
/Molecule type: DNA
/Residues: 1-277 <STO>
/Cross_references: GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB:GN00138
/Genetics:
                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                 Query Match

82.5%; Score 33; DB 2; Length 277;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 0; Indels
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earch completed: March 1, 2004, 17:36:30 ob time: 12.3333 secs

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escherichia
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                                                                                                    March 1, 2004, 17:17:25; Search time 6 Seconds (without alignments) 78:105 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P35246
Q8mb29
Q8mb20
Q8wwh0
Q8wwh0
Q8mb30
Q8
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLK7 HUMAN
FRT1 MOUSE
IHA TRIVU
PSPD BOVIN
COUG BOVIN
SNE2 HUMAN
SNE2 HUMAN
FRT1 HUMAN
TOXR VIBCH
YAOG HUMAN
APA1 MOUSE
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PAPHA
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Listing first 45 summaries
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                                                                        4 protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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equence:
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P51693 homo sapien P58461 homo sapien Q82b6 yersinia pe Q9254 homo sapien Q9954 homo sapien Q9970m0 mus musculu Q96100 homo sapien Q96100 homo sapien Q96100 homo sapien P10273 feline leuk Q8614 pan troglod P31783 bos taurus P36565 escherichia		AA. e) atum corneum chymotryptic ertebrata; Euteleostomi; Hominidae; Homo.	randt P., Carlstein A.,	atum pro	e expression of the الله الله الله الله الله الله الله الل	., Lei H., McCuaig J., serine protease gene ";	olm E., Tornell J., chymotryptic enzyme in databases.	human stratum corneum  5). intercellular cohesive  intercellular cohesive  kin in the continuous  ipecific for amino acid  Pl position. SCCE
650 1 APPI_HUMAN 666 1 NX2B_HUMAN 700 1 PTPE_HUMAN 815 1 FADE_YERPE 1007 1 CHC2_HUMAN 1049 1 ITAS_HUMAN 1292 1 CLA2_MOUSE 3298 1 PCL6_HUMAN 128 1 POL_FLV 156 1 RNP_PANTR 242 1 CD8A_BOVIN 259 1 YCBC_ECOLI	ALIGNMENTS	STANDARD; PRT; 253 AA.  1. 34, Created) 1. 42, Last sequence update) 1. 42, Last annotation update) ecursor (EC 3.4.21) (Stratum R SCCE. uman). uman). zoa; Chordata; Craniata; Verteb	, AND SEQUENCE OF 23-53.  PubMed=8034709;  Tyist M., Baeckman A., Wallbrandt	on, and characterization of e. A skin-specific human ser :19420-19426(1994).	es; las A., Diamandis B.P.; erization, mapping and tissue eum chymotryptic enzyme gene." 9) to the EMBL/GenBank/DDBJ da	SEQUENCE FROM N.A. MEDLINE=20510030; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).	SEQUENCE FROM N.A. Hansson L., Backman A., Ny A., Edlund M., Edholm E Hansson L., Backman A., Ny A., Edlund M., Edholm E Wallbrandt P., Egelrud T.; "Epidermal overexpression of stratum corneum chymo mice, a model for chronic ithchy dermatitis.", submitted (DEC-2000) to the EMBL/Genbank/DDBJ data	(19) MEDLINE=95314630; PubMed=7794273; Skyrt A., Stroemqylist M., Egglrud T.; Skyrt A., Stroemqylist M., Egglrud T.; Skyrt A., Stroemqylist M., Egglrud T.; Dischmary substrate specificity of recombinant human stratum corneum chymotryptic enzyme."; Biochem. Biophys. Res., Commun. 211:586-589(1995).  1. FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornfited layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the P1 position. SCCE
34 33 34 34 34 37 37 38 39 31 37 39 31 37 39 31 31 37 31 31 31 31 31 31 31 31 31 31 31 31 31		DJ 1  "KLX7 HUMAN STANDARD; P49862; P49862; 01-0CT-1996 (Rel. 34, Cz. 01-0CT-2003 (Rel. 34, Le. KAllikrein 7 precursor (enzyme) (RCCE) KLX7 OR PRSS6 OR SCCE. HOMO Sapiens (Human) Eukaryota; Metazóa; Ch. Mammalia; Butheria; Prin NCBI_TAXID=9606;	SEQUENCE FROM N.A., TISSUE=Skin; MEDLINE=94308225; I	Egelrud T.; "Cloning, expressic chymotryptic enzyme J. Biol. Chem. 269	12) TISSUBERCRATIONORY TOURSE (G.M., SCOTI. "Molecular characte human stratum corm Submitted (DEC-1999)	[3] SEQUENCE FROM N.A. MEDILINE-20510030; J. Gan L., Lee I., Sm. Moss P., Paeper B. "Sequenting and exp cluster located in Gene 257:119-130(2)	[4] Hanson L., Backman Wallbrandt P., Egelr "Epidermal overexpre mice; a model for ch full for ch	CHARACTERIZATION. MEDLINE-95314630; Syytt A., Stroemqu'strate Chymotryptic enzyma Biochem. Biophys!- FUNCTION: May structures in shedding of ce- residues with
		RESULT TO THE TENT	R R R R	RR RT RI	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	4

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI\_TaxID=10090;

STRAIN=C57BL/6J, TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;

SEQUENCE FROM N.A.

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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-
|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation
of precursors to inflammatory cytokines.
-!- TISSUE SPECIPICITY: Abundantly expressed in the skin and is
expressed by Kerachinocytes in the epidermis. Very low levels are
also seen in the brain and kidney.
-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels
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EMBL, AF166330; AAD49718.1; --
EMBL, AF33530; AAG33360.1; --
EMBL, AF33283; AAK69624.1; --
PIR, A53968; A55968.
HSSP, P00763; IDPO.
MEROPS; S01.300; --
GENEW, HGNC:6368; KLK7.
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253 AA;
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Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Azawa K., Izawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Saito T., Okazaki Y., Gojobori T., Baralov S., Casavant T.,
Ra Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
Rakai K., Okido T., Phuruno M., Anon H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Mune D.A., Kamiya M., Lee N. H.,
Austincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sazaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Mynshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
H., Hunctional annotation of a full-length mouse cDNA collection.";
L. Nature 409:685-690(2001).

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA STRAIN-C278BL/63; PubMed=12477932;

RA STRAIN-C278BL/64; PubMed=12477932;

RA STRAIN-C278BL/64; PubMed=12477932;

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Expleton M., Soares M.B., Bonaldo M.F., Carainoi P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carainoi P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carainoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McWany D.M., Sodergren E.J., Lu X., Gibbs R.A., Guaratache P.H.,

RA Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.W., Krzywinski M.T., Salaka U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,

ROGIGUEZ A.C., GIIMCAN, Macyaneki M.J., Salaka U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,

ROGIGUEZ A.C., GIIMCAN, Macyaneki M.J., Salaka U., Smailus D.E.,

PHOC. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

PHOC. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P20071; 1FKJ.
MGD; MGI.1913370; FKbpll.
InterPro; 1FR001179; FKBP_PPIase.
Pfam; PP00254; FKBP; 1.
PROSITE; PS00453; FKBP_PIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK003331; BAB22719.1; -. EMBL; AK019132; BAB31559.1; -. EMBL; BC037596; AAH37596.1; -.
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FRII MOUSE STANDARD; PRT; 201 AA.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
FXSO6 binding protein 11 precursor (RC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)

AESULT 2
FY11 MOUSE
FY11 MOUSE
AC Q9D1M7,
AC Q9D1M7,
AS 4-FEB
DT 15-MAR,
DT 15-MAR,
DE FK506
DE FK506
DE FK506
DE FK507

Mus musculus (Mouse)

PKBP11

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J. Mol. Endocrinol. 21:141-152(1998).

J. Mol. Endocrinol. 21:141-152(1998).

J. Mol. Endocrinol. 21:141-152(1998).

RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUTARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FINCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORNONE SECRETION,

GONADAL HORNONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

EXTHROLD DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,

ENGRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR

SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=99027340; Pubmed=9801457;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Greenwood P.J., McNatty K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomí;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
VCBI_TaxID=9337;
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INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
-i- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                 FK506 BINDING PROTEIN 11.
PPIASE FYBE.
S -> F (IN REF. 1; BAB31559).
S -> R (IN REF. 1; BAB31559).
94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                                               95.0%; Score 38; DB 1; Length 201; 88.9%; Pred. No. 2.1; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF033340, AAC63945.1; -.

GO, GO:0005576; C:extracellular, ISS.

GO, GO:0005125; F:activin inhibitor activity; ISS.

GO, GO:0005125; F:cytokine activity; ISS.

GO; GO:0003793; F:cdfenee/immunity procein activity; ISS.

GO; GO:0008183; F:acrowth factor activity; ISS.

GO; GO:0005179; F:promone activity; ISS.

GO; GO:0005515; P:procein binding; ISS.

GO; GO:0005515; P:procein binding; ISS.

GO; GO:0005159; P:procein binding; ISS.

GO; GO:0005154; P:procein differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Inhibin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 361 AA.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
ISOMERASE; RCTAMASE; SIGNAl. POTENTIAL.
                                                                                                                                     28 201 FK5
57 144 PPI
53 53
53 53
198 198 S -
201 AA; 22137 WW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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7 LLPLQLLLL 15
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Best Local Similarity
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077755;
                                                                                                                                         CHAIN
DOMAIN
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                              SEQUENCE
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LIHAY OF THAY                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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DR GO; GO:0008151; P:cell growth and/or maintenance; ISS.

GO; GO:0007166; P:cell gurface receptor linked signal transdu. .; ISS.

BR GO; GO:0007267; P:cell eurface receptor linked signal transdu. .; ISS.

BR GO; GO:0004254; P:eell-cell signaling; ISS.

BR GO; GO:0004551; P:hemoglobin biosynthesis; ISS.

BR GO; GO:0004578; P:hemoglobin biosynthesis; ISS.

BR GO; GO:004578; P:hemoglobin of apoptrosis; ISS.

BR GO; GO:004588; P:hemogliber regulation of cell cycle; ISS.

BR GO; GO:004588; P:hemogrative regulation of follicle-estimaliating. .; ISS.

BR GO; GO:004589; P:hemogrative regulation of macrophage different.

BR GO; GO:004520; P:hemogrative regulation of macrophage different.

BR GO; GO:0045226; P:hemogrative regulation of phosphorylation; ISS.

BR GO; GO:0001541; P:ovarian follicle development; ISS.

GO; GO:0001541; P:ovarian follicle development; ISS.

GO; GO:0001541; P:ovarian follicle development; ISS.

GO; GO:0001541; P:ovarian follicle development; ISS.

GO; GO:0001541; P:beta; I.

BR FRINTS; PRO0019; TGF-beta; I.

BR FRINTS; RNO0659; INHIBINA.

BR FRINTS; RNO0659; INHIBINA.

BR FROSTIE; PSO0250; TGF BETA 1; I.

BR FROSTIE; PSO025
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BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
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1-FEB-1994 (Rel. 28, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 361;
Pred. No. 3.6;
1; Mismatches 0; Indels
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MEDLINE=93170856; PubMed=8436402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 230 BY
251 361 BY
260 323 BY
289 358 BY
293 360 BY
322 360 BY
322 148 48 N-1
144 144 N-1
266 266 N-1
361 AA; 38945 MW, 1
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Best Local Similarity 88.9
Matches 8; Conservative
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PSPD_BOVIN

ID PSPD BOVIN STANDARD;

AC P35246; And 18e1. 28, Cre
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SUBUNIT: Oligomeric complex of 4 set of homotrimers (By

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HSRP, 755914; CAA53510.1; --
HSRP, 755247; 1B00.
InterPro; 1PR0018160; Collagen.
InterPro; 1PR001816; Lectin_C.
Pfam; PF01391; Collagen. 2.
Pfam; PF01391; Collagen. 2.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS000161; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface Film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat; Collage coil.
Signal: Lectin; Collagen; Repeat; Collage coil.
SIGNAL
21 369 FULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M., Skjoedt K., Holmskov U.,
"CL-46, a novel collectin highly expressed in the bovine thymus and liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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COLLED COLL (POTENTIAL).

C_TYPE LECTIN (SHORT FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

HYDROXYLATION (BY SIMILARITY).

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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collectin-46 precursor (CL-46) (46 kDa collectin).
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es 7; Conserv
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Q8MHZ9;
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DISULFID
DISULFID
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1146 BOVIN
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3T 28-FEB-
3T 28-FEB-
3D 28-FEB-
3D C011ed
3D C146.
3D Bos tan
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Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
"The cDNA cloning of conglutinin and identification of liver as a
primary site of synthesis of conglutinin in members of the Bovidae.";
Biochem. J. 292:157-162(1993).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Suzuki Y., Yin Y., Makino M., Kurimura T., Wakamiya N.;
"Cloning and sequencing of a cDNA coding for bovine conglutinin.";
Biochem. Biophys. Res. Commun. 191:335-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF509590; AAM34743.1; -.
InterPro; IPR001304; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF001391; Collagen; 2.
Pfam; PF001391; Collagen; 2.
SMART; SM00044; CLECT; 1.
PROSITE; PS00415; CTYPE LECTIN 1; 1.
PROSITE; PS50041; CTYPE LECTIN 2; 1.
Lectin; Hydroxylation; Glycoprofein; Mannose-binding; Membrane; Collagen; Repeat; Callagen; Repeat; Callagen; Repeat Collagen; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN (SHORT FORM).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCMAC. . .) (POTENTIAL).
108AC45A91420E83 CRC64;
                    85.0%; Score 34; DB 1; Length 371; 77.8%; Pred. No. 23; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONG_BOVIN STANDARD; FRT; 371 AA. P23805; 097748; 01-NOV-1991 [Rel. 20, Created) 01-D1-FBE-1994 [Rel. 28, Last sequence update) 01-OCT-1996 [Rel. 34, Last annotation update) Conglutinin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLECTIN-46.
COLLAGEN-LIKE.
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273 371 CEJ
201 203 CEJ
275 369 BY
347 361 BY
90 N N-J
371 AA; 37445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF509589; AAM34742.1;
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es 7; Conserv
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CARBOHYD
SEQUENCE
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CONG BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 21-52.
MEDLINE=87184551; PubMed=3566740;
Young N.M., Leon M.A.;
Theo marbohydrate specificity of conglutinin and its homology to proteins in the hepatic lectin family.";
Biochem. Biophys. Res. Commun. 143:645-651(1987).
-: FUNCTION: Calcium-dependent lectin-like protein which binds to a yeast cell wall extract and immune complexes through the complement component (C3bi). It is capable of binding nonreducing terminal N-acetylglucosamine, mannose, and fucose residues.
-: SUBUNIT: Oligomeric complex of 4 set of homotrimers.
-: SIMILARITY: Contains 1 Collagenous domain.
                               TISSUE=Liver;
MEDLINE=94215917; PubMed=8163202;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Liauber A.I., Sastry K.N.;
"Bovine conglutinin (BC) mRNA expressed in liver: cloning and
characterization of the BC cDNA reveals strong homology to surfactant
                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Liver,
MEDLINE-94128104; PubMed-8297370;
Kawasaki N., Itoh N., Kawasaki T.;
Kawasaki N., Itoh N., Kawasaki T.;
"Gene organization and 5.-flanking region sequence of conglutinin: a C-type mammalian lectin containing a collagen-like domain.";
Biochem. Biophys. Res. Commun. 198:597-604 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-371.
MEDILINE-91131556; PubMed=1993651;
MEDILINE-91131556; PubMed=1993651;
Lee Y.-W., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.;
"Primary structure of bovine conglutinin, a member of the C-type
                                                                                                                                                                                                                             MEDLINE=94267222; PubMed=8207234;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
"Bovine conglutinin gene exon structure reveals its evolutionary
relationship to surfactant protein-D.";
J. Immunol. 153:173-180(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal lectin family.";
J. Biol. Chem. 266:2715-2723(1991),
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JOINED.
JOINED.
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U06855; AAB60624.1; JOINED.
U06856; AAB60624.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D14085; BAA03170.1; -. EMBL; X71774; CAA50665.1; -.
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U06860; AAB60624.1;
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AAB60624.1;
                                                                                                                                          protein-D.";
Gene 141:277-281(1994).
                                                                                                                                                                                            SEQUENCE FROM N.A.
                 SEQUENCE FROM N.A.
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EMBL;
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JOINED JOINED

BAA04983.

BAA04983.2;

D25299; D25300;

EMBL; EMBL; EMBL; EMBL;

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SEQUENCE FROM N.A. (ISOFORMS 1 AND 9), FUNCTION, CHARACTERIZATION, AND
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GWKHG, GOBILS3; QBNN49; QSTER?; QBWWW3; QBWWW4; QBWWW5; QBWXH1; QBWNG4; QSYLS4; QSYLS5; QS
R EMEL; D25301; BAA04983.2; JOINED.
R PIR; 145878; 145878
R PIR; NUM450.
R PIR; NUM450.
R Interpro; 1PR008161; Clg_helix.
R Interpro; 1PR008161; Clg_helix.
R Interpro; 1PR008161; Cllagen.
R Pfam; PF001304; Lectin_C.
R Pfam; PF001304; Lectin_C:
R Prodom; PD000007; Clg_helix; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_I:
R PROSITE; PS50041; C_TYPE_RECTIN_I:
R PROSITE; PS50041; C_TYPE_RC
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HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
CELL ATTACHENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
R -> H (IN REF. 2 AND 3).
K -> S (IN REF. 2).
E -> V (IN REF. 2).
E -> V (IN REF. 2).
E -> V (IN REF. 2).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDILINE-2113122; PubMed=12118075;
MEDILINE-2213122; PubMed=12118075;
MEDILINE-27: Libotte T., Munck M., Noegel A.A., Korenbaum E.;
"NUANCE, a giant protein connecting the nucleus and actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 371;
Pred. No. 23;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM)
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MEDLINE=21652858; PubMed=11792814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONGLUTININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Sci. 115:3207-3222(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 1
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CONFLICT
SEQUENCE
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MOD_RES
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Heilig R., Eckebberg R., Petit J.-L., Fonknechten N., Da Silva C., A Cattolico L., Levy M., Barbe V., De Berardinis V., Ureta-Vidal A., Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S., Sun H., Du H., Pepin K., Artiglander L., Samson G., Cruaud C., Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P., Caraud C., Seurens B., Aniere F., Samain S., Creepeau H., Abbasi N., Alach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C., Gouyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S., Martins N., Menarins M., Manard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., A Wacherie B., Bellemere C., Belser C., Besnard-Gonnet M., Vacherie B., Bellemere C., Percon C., Lechaplais C., Louesse C., Muselet D., A Magdelenat G., Pateau E., Petit E., Sirvain-Trukniewicz P., Trybou A., Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M., Neda-Czarny N., Bataille E., Gauguet G., Roy A., Sainte-Marthe L., Werdier D., Wunderle E., Gaurpell G., Roy A., Sainte-Marthe L., Metsout E., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W., Manang J., Pether D., Waterston R., Hood L., Weissenbach J., "The DNA sequence and analysis of human chromosome 14.","
Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G., Weissberg P.L., Ellis J.A., Shanahan C.M.;
"Nesprins: a novel family of spectrin-repeat-containing proteins that localize to the nuclear membrane in multiple tissues.";
J. Cell Sci. 114:4485-4498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 1-956 AND 5133-6885
                                                                                                                        MEDLINE=22296883; Pubmed=1248964; Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.; The mesprine are giant actin-binding proceins, orthologous to brosophila melanogaster muscle protein MSP-300."; Genomics 80:473-481(2002).
                                                                                                                                                                                                                                                                      Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A: (ISOFORM 8).
                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                              OUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              [5]
SEQUENCE FROM N.7
PubMed=12508121;
                                                                                                                                                                                                                                                         rissum=Testis;
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Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O., Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Eurnya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta T., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,

TISSUE=Spleen, and Tongue;

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Isold=Q8WXH0-8; Sequence=VSP_007161, VSP_007162;
Note=No experimental confirmation available;
Name=9; SynonymesNUANCE-N-13;
Isold=O8WXH0-9; Sequence-VSP_007159, VSP_007160;
-!- TISSUE SPECIFICITY: Widely expressed, with higher level in kidney,
                                                                                                                                                                                                                   MEDLINE=99246063; PubMed=10231032; Nagare M., Kikuno R., Hirosawa M., Nagase T., Ishikawa K.I., Suyama M., Kikuno R., Hirosawa M., Mayase T., Tanaka A., Kocani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; pNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Involved in the maintenance of nuclear organization and structural integrity. Probable anchoring protein which theters the nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton by interacting with the nuclear envelope and with F-actin in the
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=22158633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Chara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA clones.";
DNA Res. 9:99-106(2002).
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawata-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=Produced by exon skipping that results in a frameshift. No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The largest part of the protein is eyropleamic, while its C-terminal part is associated with the nuclear envelope, most probably the outer nuclear membrane. Remains associated with the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSP 007165, VSP 007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8WXH0-5; Sequence=VSP_007157, VSP_007164, VSP_007165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECURNCE OF 5754-6885 FROM N.A.
MEDLINE-21154917, PubMed=11230166,
Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterrhoeft A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwalder B., Obermaier B., Tampe J., Heubner D.,
Wambutt R., Korn B., Klein M., Poustka A.,
Trowards a catalog of human genes and proteins: sequencing and
analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoplasm.
SUBUNIT: Interacts with F-actin via its N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2;
IsoId=Q8WXH0-2; Sequence=VSP_007164, VSP_007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=Q8WXH0-7; Sequence=VSP_007154, VSP_007163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope during its breakdown in mitotic cells.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q8WXH0-6; Sequence=VSP_007158, VSP_007
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=9;
                                                                                                                                                                             SEQUENCE OF 5709-6885 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lsoId=Q8WXH0-3; Sequence=VSP 007155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=Q8WXHO-4; Sequence=VSP_007156;
me=5; Synonyms=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId≂Q8WXH0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synonyms=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=4; Synonyms=Beta;
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                                                                                                                                                                                                                                                                                                                                                                                                           SNEI HUMAN STANDARD; PRT; 8797 AA.

GRNF91, 094690; QRNP97; QRNCPI; QRNWW6; QRWW7; QRWXF6; Q96NIJ;
Q9C0A7; Q9H525; Q9H526; Q9NS36; Q9NU36; Q9UJ06; Q9UJ07; Q9ULF8;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nesprin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Myocyte nuclear envelope protein 1) (Myne-1) (Enaptin 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESTS OF 8758-LEU--CYS-8763.

MUTAGENESTS OF 8758-LEU--CYS-8763.

TISSUE-Heart, Placenta, Skeletal muscle, Spleen, and Testis;

MEDLINE-21652888; PubMed-11722814;

Zhang Q., Skepper J.N., Yang P., Davies J.D., Hegyi L., Roberts R.G., Weissberg P.L., Ellis J.A., Shanahan C.M.;

"Nesprins: a novel family of spectrin-repeat-containing proteins that localize to the nuclear membrane in multiple tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 34; DB 1; Length 6885;
87.5%; Pred. No. 4e+02;
ive 1; Mismatches 0; Indels 0; Gaps
adult and fetal liver, stomach and placenta. Weakly expressed in skeletal muscle and brain. Isoform 5 is highly expressed in pancreas, skeletal muscle and heart.

DOMAIN: The Klarsicht domain mediates the nuclear envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Heart, Spleen, and Testis;
MRDLINE-22296931; PubMed-12409964;
Shang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
"The nesprins are giant actin-binding proceins, orthologous to
Drosophila melanogaster muscle protein MSP-300.";
Genomics 80:473-481 (2002).
                                                                                                 -i. SIMILARITY: Belongs to the nesprin family.
-i. SIMILARITY: Contains 1 actin-binding domain.
-i. SIMILARITY: Contains 2 calponin-homology (CH) domains.
-i. SIMILARITY: Contains 1 Klarsicht domain.
-i. SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
-i. SIMILARITY: Contains 9 spectrin repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR KIAA0796 OR KIAA1756 OR KIAA1262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF495911; AANG0443.1; -.
EMBL, AL117404; CABS590S.1; -.
EMBL, AL1162832; -; NOT ANNOTATED CDS.
EMBL, AL355094; -; NOT ANNOTATED_CDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF435010, AAL33547.1; -- EMBL, AF435011, AAL33548.1; -- EMBL, AY061757, AAL33800.1; -- EMBL, AY061758, AAL33801.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY061758; AAL33801.1
EMBL; AY061759; AAL33802.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
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Best Local Similarity
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Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.,
"Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:347-355(2000).
                                                                    "The longest isoform of enaptin/Syne-1, a nuclear envelope associated protein, binds actin cytoskeleton via the alpha-actinin-like actin-binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Adrenal gland, and Teratocarcinoma;
Ninomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
Kausuti T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Ximura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
Nagai K., Isogai T.,
Nagai K., Isogai T.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Erain;
MEDLINE=99087487; PubNed=9872452;
NGDLINE=99087487; PubNed=9872452;
NGDREST. Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Almeda J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M., Tracey A., Williams S., Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                            Braune S., Abraham S., Padmakumar V., Tunggal B., Noegel A.A., Korenbaum E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20039619; Pubmed-10574462;
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
Gough L., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.;
"Golgi localization of syne-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ansorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
Zhang Q., Shanahan C.M.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 6922-8797 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-856 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [12]
REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara O.;
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SEQUENCE OF 8406-8797 FROM N.A.

Ma F.-R., Zhu L.-P.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) to the maintenance of nuclear organization and structural integrity. Probable anchoring protein which theters the nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton. Connects nuclei to the cytoskeleton by interacting with the nuclear envelope and with F-actin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=08NF91-9; Sequence=VSP 007133, VSP 007143, VSP 007144; TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal and smooth muscles, heart, spleen, and peripheral blood
                                                                                                                                      SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.
MEDLINE=21659781; PubMed=11801724;
Mislow J.M.K., Kim M.S., Davis D.B., McNally E.M.;
Myne-1, a spectrin repeat transmembrane protein of the myocyte inner
muclear membrane, interacts with lamin A/C.";
J. Cell Sci. 115:61-70(2002).
             MEDLINE=2215633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                     o'toplasm.

-!-SUBURIT. Interacts with MUSK, with F-actin via its N-terminal domain, and with LMMA in vitro (By similarity).
-!-SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The largest part of the protein is gyroplasmic, while its C-terminal part is associated with the nuclear envelope, most probably the outer nuclear membrane. In skeletal and smooth muscles, a significant amount is found in the sarcomeres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prediction.
CAUTION: Ref.7 (BAB71097) sequence differs from that shown due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoid=Q8NF91-4; Sequence=VSP_007134, VSP_007139, VSP_007140,
VSP_007144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- DOWAIN: The Klarsicht domain, which contains a transmembrane domain, mediates the nuclear envelope targeting.
-1- SIMILARITY: Belongs to the nesprin family.
-1- SIMILARITY: Contains 1 actin-binding domain.
-1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
-1- SIMILARITY: Contains 12 HAT repeats.
-1- SIMILARITY: Contains 1 Klarsicht domain.
-1- SIMILARITY: Contains 31 spectiful repeats.
-1- CAUTION: Ref. 5 (CAB55865, CAB55866, CAC16280 and CAC16281)
-1- CAUTION: Ref. 5 (CAB55865, CAB55866, CAC16280 and CAC16281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Ref.14 sequence differs from that shown due to two frameshifts in positions 8412 and 8784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=2; Synonyms=Beta;
IsoId=Q8NF91-2; Sequence=VSP_007130;
Name=3; Synonyms=Alpha;
IsoId=Q8NF91-3; Sequence=VSP_007132, VSP_007144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q8NF91-5; Sequence=VSP_007135, VSP_007136;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q8NF91-7; Sequence=VSP_007141, VSP_007142;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q8NF91-6; Sequence=VSP_007137, VSP_007138;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=8; Synonyms=Beta 2;
IsoId=Q8NF91-8; Sequence=VSP_007131;
Name=9; Synonyms=Alpha 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q8NF91-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric cDNA.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
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TISSUE FROM NA.

TISSUE FROM NA.

REDINE=2388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

REDINE=22388257; PubMed=12477932;

RALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K.H., Ramer A.A., Rubin G.M., Hong L.,

A Explecton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellann N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McWarn P.J., McKernan K.J., Malek J.A., Gunsarene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahy, Willing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahiting W., Touchman J.W., Green E.D., Dickson M.C.,

Rahiting W., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
FKS06 binding protein | Precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FKS06-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 8797;
Pred. No. 5.1e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rulten S., Kay J.E., Robinson C.;
"Identification of novel FKBP genes.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                           EMBL, AY061755, AAL33798.1; -.
EMBL, AY061756, AAL33799.1; -.
EMBL, AF495910, AAN60442.1; -.
EMBL, AF535142; AAN03486.1; -.
EMBL, AY184203; AAO27771.1; -.
EMBL, AY184206; AAO27774.1; -.
EMBL, AL049548; CAB55865.1; AL049548; CAB55866.1; -.
EMBL, AL049548; CAB87586.1; -.
                                                                                                                                                                                                                                                                                                                            AL136079; NOT ANNOTATED CDS.
AL138832; CAC16280.1; ALT SEQ.
AL138832; CAC16281.1; ALT SEQ.
AL357081; NOT ANNOTATED CDS.
AL560401; NOT ANNOTATED CDS.
AL589963; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8749 LPLQLLLL 8756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LPLQILLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKBP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKBP11 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
FK11_HUMAN
                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
EMBL;
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190 LLPLAVLLL 198
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     SOLUTION NO DESCRIBILITATION NO DESCRIBIRADA NO DE
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-20406833; PubMed=10952301;
Heidelberg U.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                     protein synthesis.
-i- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Classical 569B / ATCC 25870 / Serotype Ol;
MEDLINE=81102874; PubMed=3802195;
MAIler V.L., Taylor R.K., Mekalanos J.J.;
"Cholera toxin transcriptional activator toxR is a transmembrane DNA
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U. S.A. 99:16899-16903(2002).
-!- FUNCTION: PPlases accelerate the folding of proteins during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria; Gammaproteobacteria, Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.5%; Score 33; DB 1; Length 201; 77.8%; Pred. No. 20; tive 1; Mismatches 1; Indels
                                                                                                                                                                               -!- SIMILARITY: Belongs to the FKBP-type PPlase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AA; 22180 MW; 586E430B9D2DC0A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. FK506 BINDING PROTEIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPIASE, FKBP-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P15795; Q9KTB9; 01-APR-1990 (Rel. 14, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cholera toxin transcriptional activator. TOXR OR VC0984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; FALSE NEG.
PROSITE; PS50059; FKBP PPIASE 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q00688; 1PBK.
Genew; HGNC118624; FKBP11.
InterPro; 1PR001179; FKBP_PPIase.
Pfam; PF002254; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF238079; AAF63478.1; -. EMBL; BC027973; AAH27973.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isomerase; Rotamase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 7/....
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Cell 48:271-279(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LIPINLLLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LLPLQILLL 9
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                                                                                                                                                        (omega=0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTCEMBAIN K.M., Dirita V.J., Mekalanos J.J.;

"TOAR Proteins with substitutions in residues conserved with OmpR
fail to activate transcription from the cholera toxin promoter.";
J. Bacteriol. 174:6807-6814(1992).
-! FUNCTION: THIS TRANSCRIPTION ACTIVATOR CONTROLS CHOLERA TOXIN,
VIBRIO CHOLERAE. IT BINDS TO THE 5'-TITIGAT-3' TANDEMLY REPEATED
DNA SEQUENCE IN CHOLERA TOXIN PRONOTER REGION. TOXS. INTERACTS WITH
THE C-TERMINAL PERIPLASMIC DOMAIN OF TOXR, STIMULATING ITS
ACTIVITY. IT ACTIVATES TRANSCRIPTION AT THE PROMOTERS FOR TCPI AND
TCPA AND THIS IS PRESUMABLY VIA FORT.
-!- SIMILARITY: TO B. COLI CADC, AND TO THE C-TERMINI OF A GROUP OF
TRANSCRIPTIONAL ACTIVATORS (OMPR-LIKE PROTEINS).
                                                                                                                                                                                                                                      Parsot C., Mekalanos J.J.,
"Expression of ToxR, the transcriptional activator of the virulence
factors in Vibrio cholerae, is modulated by the heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 263-294 PROM N.A. MEDILINE-91098611; PubMed-1898871; Dirita V.J., Mekalanos J.J., Dirita V.J., Mekalanos J.D., Periplasmic interaction between two membrane regulatory proteins, ToxR and ToxS, results in signal transduction and transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR, VC0984; -.
Interbro, IPR001867; Trans_reg_C.
Interbro, IPR004867; Trans_reg_C.
Probom; P000485; Trans_reg_C; 1.
Probom; P0001929; Trans_reg_C; 1.
Transcription regulation; DNA-binding; Activator; Transmembrane;
Trans-acting factor; Complete proteome.
Trans-acting factor; Complete Droteome.
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Pred. No. 29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 294 PERPELASMIC (POTENTIAL).
134 134 S -> N (IN REF. 1).
172 T -> A (IN REF. 1).
184 L -> F (IN REF. 1).
204 204 T -> S (IN REF. 1).
294 AA, 32506 MW, 15EF85EA653C373E CRC64;
                                                                                                                                                                                                                                                                                                                                                  response.";
Proc. Natl. Acad. Sci. U.S.A. 87:9898-9902(1990).
                                                                                                                                  SEQUENCE OF 1-11 FROM N.A.
STRAIN-El Tor E7946;
MEDLINE-91088618; PubMed=2124707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93015740; PubMed=1400230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004179; AAP94145.1; -.
EMBL; MS8033; AAA27575.1; -.
EMBL; M62761; AAA63558.1; -.
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77.8%;
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                                                                      Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8
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PIR; E82257; E82257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation."
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Hypothetical protein.
NON TER 1 1
NON TER 500 500
SEQUENCE 500 AA; 58
                                                                                                                                                                                                                                                                                                                                                                            363 LVPLQILL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                   1 LLPLOILL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLAGEN-BINDING.
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844X8886666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 435;
Pred. No. 42;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khodes S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databaees.
-!- SIMILARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knodes 8.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                                                                                                                                                           Grafham D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grafham D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 AA; 50539 MW; 3D19443032BBB494 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein D4845024.2 (Fragment)
Homo sapiens (Human)
                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                 Hypothetical protein DJ845024.5 (Fragment)
Homo sapiens (Human).
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Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                        STANDARD;
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NON TER 435 43
SEQUENCE 435 AA; 5
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                                                                                        HUMAN
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BR MRMI, ALOZGOIN COALISTI.

THY NOW TERR 101 COALISTI.

WHYCHARD SIGNARIA 233.1;

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**MEDLINE=22113598; PubMed=12228233; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-seretase regulates transcription."; J. Biol. Chem. 277:44195-44201(2002).

J. Biol. Chem. 277:44195-44201(2002).

General Chem. 277:44195-44201(2002).

Gamma-secretase processed fragment, ALIDI, activates transcription activation through APBBI (Fe65) binding. Couples to JIP signal transduction through C-terminal binding. May interact with cellular G-protein signaling pathways. Can regulate neurite outgrowth through binding pathways. Can regulate neurite outgrowth through binding to components of the extracellular cellular G-protein signaling pathways. Can regulate neurite cellular gamma-CTF peptide, C30, is a potent enhancer of neuronal apoptosis (By similarity).

J. SUBMITT Binds, Via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB and APBB family members, MAPKBIP1 and Dabl (By similarity). Binding to Dabl inhibits its serine phosphorylation.

J. SUBCELULAR LOCATION: Type I membrane protein. C-terminally processed in the Golgi complex.

J. DOMAIN: The NRYX sequence motif found in many tyrosine-
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   GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBEL, AND MUTAGENESIS OF
  MEDLINE=99389880; PubMed=10460257;
Homayouni R., Rice D.S., Sheldon M., Curran T.;
"Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
   -!- PTM: N- and O-glycosylated.
-!- MISCELLANFOUS: Binds zinc and copper in the extracellular domain.
Zinc-binding increases heparin binding. No Cu(II) reducing activity with copper-binding.
-!- SIMILARITY: Belongs to the APP family.
  phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The NPXY site is also involved in clathrin-mediated
  MEDLINE=21408156; PubMed=11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T., Hirai S., Ohno S., Kaviaki Y., Kawasumi M., Kouyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.; Kyriakis J.M., Nishimoto I.; Mariakis J.M., Nishimoto I.; Kariakis J.M., Nishimoto I.; Mariakis J.M., Nishimoto I.; Mariakis J.M., Nishimoto I.; Jinko J. Lerminal Kinase (JNK) interacting protein-1b/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).
   -!- PTM: Proteclytically cleaved by caspases during neuronal apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
  J. Neurosci. 19:7507-7515(1999).
  AAH21877.1; -.
  EMBL; L04538; AAA37247.1;
EMBL; BC021877; AAH21877.1
   INTERACTION WITH MAPKSIP1
[4]
INTERACTION WITH DABL,
   endocytosis
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PIR, A46362; A46382. HSSP, P05067; IMWP. MGD; MGI:88046; Aplpl. InterPro; IPR008155; A4\_APP. Interpro; IPR008155; A4\_EXTRA.

SMART; SM00006; A4\_EXTRA; 1. PROSITE; PS00319; A4\_EXTRA; 1 PR00203; AMYLOIDA4.

PRINTS;

```
RADIATOR FROM N.A.

RADIATOR Y. Karnik S., Husain A.;

Liao Y., Karnik S., Husain A.;

Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.

Liao Y. Warnik S., Husain A.;

Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.

Toles in vasoactive peptide generation, extracellular matrix

C. -- CATALYTIC ACTIVITY: Preferential cleavage: Phe-|-kaa > Tyr-|-kaa >

Trp-|-xaa > Leu-|-xaa.

C. -- SARGELIULAR LOCATIVITY: Preferential cleavage: Phe-|-kaa > Tyr-|-xaa >

Trp-|-xaa > Leu-|-xaa.

C. -- SUBCELIULAR LOCATIVITY: Belongs to peptidase family S1. Granzyme subfamily.

C. -- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.

C. -- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.

C. -- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.

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C. -- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily S1. Granzyme subfamily S1. Granzyme subfamily S1.
  SIMILARITY).
CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
  Gaps
PROSITE; PS00120; A4 INTRA; 1.
Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
  REQUIRED FOR COPPER(II) REDUCTION (BY
   Papio hamadryas (Hamadryas baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Y-G: REDUCED BINDING OF APBB1.
P -> PP (IN REF. 2).
56516DG3EA40E4B0 CRC64;
  COPPER-BINDING.
ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
   BASOLATERAL SORTING SIGNAL (BY
  82.5%; Score 33; DB 1; Length 653; 77.8%; Pred. No. 63; 1; Mismatches 1; Indels
   MCT1 PAPHA STANDARD; PRT; 247 AA.

1D MCT1_PAPHA STANDARD; PRT; 247 AA.

2 P52195;

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 28-FE22003 (Rel. 41, Last annotation update)

DE Chymase precursor (EC 3.4.21.39) (Mast cell protease I).

GN CMAI OR CHM.
  AMYLOID-LIKE PROTEIN 1.
C30 (BY SIMILARITY).
EXTRACELLULAR (POTENTIAL).
  CYTOPLASMIC (POTENTIAL).
  POTENTIAL.
  72750 MW;
   Local Similarity 77.8
   Cercopithecinae; Papio.
NCBI_TaxID=9557;
   22 tipistiti 30
  1 LLPLQILLL 9
   643
4643
554
554
641
653 AA;
   Glycoprotein.
SIGNAL
  CHAIN
DOMAIN
TRANSMEM
DOMAIN
  CARBOHYD
MUTAGEN
CONFLICT
  CARBOHYD
  SEQUENCE
   Query Match
   DOMAIN
   DOMAIN
  DOMAIN
   DOMAIN
  DOMAIN
   SITE
        SO THE FETT 
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0
   cavity of adult P.americana.
-! MISCELLANBOUS: Calcium is required for lipopolysaccharide binding.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
  "DEGL" Chem. 266:13318-13323(1991).
-!- FUNCTION: Participates probably in the elimination of foreign elbstances invading the insect abdominal cavity, and in trapping intracellular symbionts, when they leak from the mycetomes into
  ESQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE=Hemolymph;
MEDILINE=91302364;
Demori T., Natori S.;
"Molecular cloning of cDNA for lipopolysaccharide-binding protein from the hemolymph of the American cockroach, Periplaneta americana. Similarity of the protein which animal lectins and its acute phase expression...;
  Gaps
  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
Hemolymph lippoplysaccharide-binding protein precursor (LPS-binding protein) (LPS-B)
Periplaneta americana (American cockroach)
Periplaneta, Merazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Blattidae, Periplaneta.
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
NORI_TAXID=6978;
  the hemolymph.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECITY: Hemolymph.
-!- INDUCTION: By introduction of foreign cells into the abdominal cavity of adult P.americana.
  CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
WAY, EGECISEOFA72FD8B CRC64;
  .
0
EMBL; U38521; AAA91150.1; --
EMBL; U3846; AAA91150.1; --
HSRP; P23946; IKLT.
MEROPS; P2140; --
InterPro; IPR001234; Peptidase_S1A.
INTERPRO; ITYPESIN. 1.
PROSITE; PS00204; TRYPESIN. 1.
PROSITE; PS00135; TRYPESIN_SER; 1.
   80.0%; Score 32; DB 1; Length 247; 77.8%; Pred. No. 38; 1; Indels ive 1; Mismatches 1; Indels
  256 AA.
  CHYMASE
  PRT;
   188 BY
80 N-
103 N-
27339 MW;
   STANDARD;
  Conservative
  3 LLPLPLLL 11
   σ
  Similarity
7; Conserva
  80
103
247 AA;
  1 LLPLOILLL
  LPSB PERAM P26305;
  Query Match
Best Local S:
Matches 7
   ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
   CARBOHYD
CARBOHYD
  SEQUENCE
  SIGNAL
PROPEP
CHAIN
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
  Gaps
   HEMOLYMPH LIPOPOLYSACCHARIDE-BINDING
   (PROBABLE)
  ô
   Score 32; DB 1; Length 256;
Pred. No. 40;
2; Mismatches 1; Indels
  C-TYPE LECTIN (SHORT FORM)
BY SIMILARITY.
BY SIMILARITY.
; EBDF74F1AEG39858 CRC64;
  N-LINKED (GLCNAC.
   EMBL; D00711; BAA00616.1; -
PIR; A39873; JQ0708.
HSSP; P20693; 1HLJ.
HSSP; P20693; 1HLJ.
PRAMT; SM00039; lectin_c; 1.
SWART; SM00034; CLECT; 1.
PROSITE; PS00415; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Lectin; Signal; Calcium.
  POTENTIAL
   28420 MW;
  80.0%;
   Conservative
   256 AA;
  Similarity 6; Conserv
   Glycoprotein; I
SIGNAL
PROPEP 22
CHAIN 34
  DISULFID
DISULFID
SEQUENCE
   Query Match
Best Local S
  CARBOHYD
   DOMAIN
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Search completed: March 1, 2004, 17:29:58 Job time : 7 secs

1 LLPLOILLE 9 |||| :||: 7 LLPLSVLLM 15

8 8

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QBn5n9 homo sapien
QBvca9 mus musculu
QBr566 mus musculu
QBv566 mus musculu
QBv7n5 clostridium
QBnz20 helicoverpa
Q215.7 clethrionom
QBimf1 drosophila
Q95kg5 helicobacte
Q8m3y6 manestra br
Q95kg5 helicobacte
Q8m3y6 manestra br
Q8m2y6 spodoptera
Q8mzv6 spodoptera
Q8mzv6 spodoptera
Q8mzv6 spodoptera
Q7vht6 helicobacte
Q7vht6 helicobacte
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   March 1, 2004, 17:20:41 ; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
  Description
   1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
   otal number of hits satisfying chosen parameters:
  1017041 segs, 315518202 residues
   SUMMARIES
   ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  M protein - protein search, using sw model
   Q8N5N9
Q8VCA9
Q8N5D6
Q8NB59
Q97H76
Q8MZZ0
Q21527
Q81MF1
Q92KQ5
   Q8MZZ6
Q7VHT6
Q922G5
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   sp_rodent:*
sp_virus:*
sp_virus:*
sp_unclassified:*
sp_roinus:*
sp_bacteriap:*
sp_archeap:*
  Q8MZX7
Q8MZV6
  QBMZY6
   SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_tungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_amaxi:*

7: sp_mhc:*
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| 20222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |           | ULLT 1  SOUSN9  DEBLIMINARY,  DONNSN9  OBNISN9;  OLOCT-2002 (TERMELTE1. 22, Lest  OLOCT-2002 (TERMELTE1. 25, Lest  OLOCT-2003 (TERMELTE1. 25, Lest  Mallikrein 7 (Chymotryptic, strat Homo sapiens (Human).  DENKATYPOTA, Metazoa; (Dordata; Cra Mammala; Butheria; Primates; Car  NCBI_TAXID=9606;  Ill  SEQUENCE FROM N.A.  TISSUE-Skin;  SUBMILED (UNN-2002) to the EMBL,  -1- SIMILARTY: BELONGS TO PEPTII  EMBL; BCO32005; AMH32005.1; -00; GO:0004205; F:Chymotrypsin activ  GO; GO:0004205; F:Chymotrypsin activ  GO; GO:0004205; F:Crypsin activ  GO; GO:0004205; F:trypsin activ  EMBL; BROONSS; T:Trypsin 1.  PROSITE; PROONSS; T:Trypsin; 1.  PROSITE; PROONSS; T:TYPSIN ISS.1.  PROSITE; PROCESS; T:TYPSIN ISS.1.  PROSITE; PROONSS; T:TYPSIN ISS.1.  PROSITE; PROONSS; T:TYPSIN ISS.1.  PROSITE; PROONSS; T:TYPSIN ISS.1.  PROSITE; PROONSS; T:TYPSIN ISS.1.  PROCESS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROCESS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROCESS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.  PROONSS T:TYPSIN ISS.1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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Query Match
  CAC2137
  97H76Q
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   7H76
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   Gaps
  Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN cDNA 1110002023 gene.
MNS musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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   95.0%; Score 38; DB 11; Length 104; 88.9%; Pred. No. 4.8; 1ive 1; Mismatches 0; Indels
   Match 95.0%; Score 38; DB 11; Length 73; Local Similarity 88.9%; Pred. No. 3.5; es 8; Conservative 1; Mismatches 0; Indels
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TISSUE-Salivary gland;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1;
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
  Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022990. AAH22900.1; -.
MGD; MGI:1913370; FKbp11.
  GO; GO:006457; P:protein folding; IEA.
InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
PROSITE; PS0043; FKBP PPIASE 1; 1.
PROSITE; PS50059; FKBP PPIASE 1; 1.
SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN CDNA 1110002023 gene.
FKBP11 OR 1110002023RIK.
  79 AA.
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Matches 8; Conservative
   PRELIMINARY;
   PRELIMINARY;
  PRELIMINARY;
  7 LLPLOLLL 15
                 6 LLPLQILLL 14
1 LLPLQILLL 9
  1 LLPLQILLL 9
  1 LLPLQILLL 9
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
  Query Match
Best Local S:
Matches 8
   Q8VCA9
  Q8VB59
Q8VB59;
   ESULT 4
)8VB59
ID Q8VB9
  ESULT 3
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STRAIN=Taiwan,
MEDLINE=21844071; PubMed=11853398;
Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.,
"Identification of a nucleocapsid protein (VP35) gene of shrimp white
spot syndrome virus and characterization of the motif important for
targeting VP35 to the nuclei of transfected insect cells.";
Virology 293:44-53(2002).
   syndrome
  Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
   STRAIN=Taiwan;
MEDINE=20517548; PubMed=11062040;
MEDINE=20517548; PubMed=11062040;
Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot syndyrive (MSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
   ;
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   SEQUENCE FROM N.A. PubMed=11689662; MEDINE=2154811; VARION F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.; "Complete genome sequence of the shrimp white spot bacilliform
   90.0%; Score 36; DB 12; Length 79; 77.8%; Pred. No. 9.5; tive 2; Mismatches 0; Indels
   SEQUENCE FROM N.A.
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
   01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cation transport P-type ATPase.
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
WSV132 (WSSV187).
   White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
NCBI_TaxID=92652;
   845 AA
   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
   PRT;
  virus.";
J. Virol. 75:11811-11820(2001).
[2]
   Local Similarity 77.8
tes 7; Conservative
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   1 LLPLQILLL 9
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=1488;
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Query Match

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Best Local Similarity 87.5%; Pred. No. 33;
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NON TER 1 1 1
NON_TER 183 183
SEQUENCE 183 AA; 21196 MW; 72
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   SEQUENCE
   021527
021527;
   CG31600
   QBIMF1
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021527
   RESULT 8
  Q8IMF.
   ò
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing J. Bacterium Clostridium acetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing J. Bacteriol. 183:4823-4838(2001).

EMBL; AB007114; AAK80095.1; -.

EMBL; AB007114; AAK80095.1; -.

GO; GO:0016020; C::membrane; IEA.

GO; GO:0016021; F:ATP binding; IEA.

GO; GO:001672; F:ATP ace activity; IEA.

GO; GO:001672; F:ATP binding; IEA.

GO; GO:001673; F:Hydrolase activity; IEA.

GO; GO:001673; F:Hydrolase activity; IEA.

GO; GO:001673; F:Hydrolase activity; IEA.

GO; GO:001673; F:Hydrolase EI-E2.

R InterPro: IPR00159; A:Papase.

R InterPro: IPR00689; Cation ATPase.

R InterPro: IPR00689; H.ATPase.

R Pfam; PF00689; Cation ATPase.

R Pfam; PF00689; Cation ATPase.

R Pfam; PF00689; Cation ATPase.

R Pfam; PF00122; EI-E2 ATPase.

R Pfam; PF00122; EI-E2 ATPase.

R Pfam; PF00122; HATPASE.

R Pfam; PF00122; HATPASE.

R Pfam; PF00122; HATPASE.

R Pfam; PF00122; HATPASE.
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   Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;

"Byolution of the Integral Membrane Desaturase Gene Family in Moths
"Byolution of the Integral Membrane Desaturase Gene Family in Moths
"By Damitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF842910; AAN28485.1;

EMBL, AF842910; AAN28485.1;

R GO; GO:0005020; C:membrane; IEA.

R GO; GO:0005020; C:membrane; IEA.

R GO; GO:00064769; F:stearoyl-CoA 9-desaturase activity; IEA.

R GO; GO:00064769; F:stearoyl-CoA 9-desaturase activity; IEA.

R GO; GO:00064769; F:stearoyl-CoA 9-desaturase activity; IEA.

R InterPro; IPRO01521; Posaturase.

R InterPro; IPRO05804; FA desaturase.

R Ffam; PF00487; FA desaturase.

R Pfam; PF00487; FA desaturase.
   Acyl-CoA desaturase (Fragment).
Helicoverpa assulta (Oriental tobacco budworm).
Bukaryota; Matazaa; Arthropoda; Hexapoda; Insecta; Pterygota;
Mocytera; Endopterygota; Lepidoptera; Glossata; Ditrysla; Noctuoidea;
Noctuidae; Helicthinae; Helicoverpa.
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  90.0%; Score 36; DB 16; Length 845; 77.8%; Pred. No. 86;
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  01-0CT-2002 (TrEMBLrel. 22, Created)
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PRINTS; PR0120; HATPASE.
TIGREAMS; TIGR01494; ATPASE P-type; 5.
Complete proceome.
SEQUENCE 845 AA; 93779 MW; 401293A
  Pfam; PF00487; FA desaturase;
PRINTS; PR00075; FACDDSATRASE.
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   Local Similarity 77.8
nes 7; Conservative
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  1 LLPLOILL 9
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   STRAIN=PPAE;
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   QBMZZ0
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Matches
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28MZZO

200 MZZ

1.C QGMZZ

200 MZ

201 MZ

201 MZ

202 MZ

203 MZ

204 MZ

205 MZ

206 MZ

207 MZ

207 MZ

208 MZ
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  Molecular systematics and processing  Gaps
   MEDLINE=99152303; PubMed=9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Arvicolinae,
   ö
   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH debydrogenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain 4) (Fragment).
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  Clethrionomys gapperi (Southern red-backed vole).
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PRINTS; PR01437; NUOXDRDTASE4.
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PRT;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adamanatides P. G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutron G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,

Nan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

Abril J.F., Agbayani A., An H.J., Andrews-Pénnkoch C. Baldwin D.,

Ballew R.M., Bence P.V., Berman B.P., Bandari D., Bolhakov S.,

Berson K.Y., Bence P.V., Berman B.P., Bandari D., Bolhakov S.,

Borkova D., Botcher M.R., Bouck J., Broketein P., Etchier P.,

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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

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Spier E., Spradiing A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradiing A.C., Stapleton M., Stupski M.P., Smith H.O.,

Alber S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Alber S.M., Wordager, Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

Alber S.M., Wordager, Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

Spience Sequence of Drosophila melanogaster.",

Science 287:2185-2195(2000).
  SEQUENCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Relniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reritara S., Frise E., Calle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

McDeyam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McDeyam C., Dark S., Patel S., Patel S., Petelffer B.,

Rouanenavong S., Pittman G.S., Patel S., Patel S., Patelffer B.,

Milliams S.M., Zaveri J.S., Smith H.O., Vener J.C., Rubin G.M.,

Supmitted (MAR-2000) to the BMBL/GenBank/DDBJ databases.
  Hista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Rusch S. Sazle S.M., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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  MEDLINE=99120557; PubMed=9921682; Alm R.A., Ling L.,, Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Carmeo A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
  Gaps
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   "Genomic sequence comparison of two unrelated isolates of the human agartic pathogen Helicobacter pylori.";
Nature 397:176-180(199)
EMBL; AE001518; AAD06464.1; -.
  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
  ó
              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
   PIR; A71875; A71875.

QO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015385; F:scadium:hydrogen antiporter activity; IEA.

GO; GO:0006885; P:regulation of pH; IEA.

InterPro; IPR04770; Antiport_nhaC.

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FlyBase, FBGH0051600; CG31600.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved hypothetical integral membrane protein.
   493 AA.
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Matches 8; Conservative
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   PRELIMINARY;
  254 Libisitii 262
  |:|||||:|
77 LIPLQILVL 85
  1 LLPLQILLL 9
   1 LLPLOILLL 9
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
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AC 025600
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  RESULT 9
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ProDom; PD002221; Desaturase; 1.
  SEQUENCE FROM N.A.
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SEQUENCE
                            NON TER
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SEQUENCE
   Query Match
  Q8MZX7
   O8MZV6
  Best Loc
Matches
  RESULT 13
   RESULT 12
   O8MZX7
  d
   SX OCCOSE DE LA SE
   C. STRAIN=LPAG;

K. MIDDED D.C., Rosenfield C.L., You K.M., Jeong S.E.;

R. MIDDED D.C., Rosenfield C.L., You K.W., Jeong S.E.;

"Evolution of the Integral Membrane Desaturase Gene Family in Moths and Flies.";

"Evolution of the EMBL/GenBank/DDBJ databases.

R. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF482914; AAM28489.1;

R. GO; GO:0005783; C:endoplasmic reticulum; IEA.

GO; GO:0016783; C:endoplasmic reticulum; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

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GO; GO:0016526; F:iron ion binding; IEA.

GO; GO:0016531; F:farty acid biosynthesis; IEA.

R. GO; GO:0006633; P:farty acid biosynthesis; IEA.

R. InterPro; IPRO01822; Desaturase.

R. R. InterPro; IPRO01804; F.A. desaturase.

R. PERINTS; PRO0075; FACBSATRASE.

R. PRINTS; PRO0075; FACBSATRASE.
  STAAIN=26695 / ATCC 700392;
STAAIN=26695 / ATCC 700392;
MEDLINE=97394467; Pubmed=9252185;
Tomb J.-F., White D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Releschmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodgon H.C., Khalak H.G., Glodek A., Kchaney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Walter J.C.;

Wenter J.C.;
   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea, Noctuidae, Hadeninae, Mamestra.
   Gaps
                                Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
   "The complete genome sequence of the gastric pathogen Helicobacter
   ö
   pylori.";

Wature 388:539-547(1997).

EMBL; AE000604; AAD07993.1; -.

PIR; B64638; B64638.

TIGR; HP0946; -.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0015385; F:sedium:hydrogen antiporter activity; IEA.

GO; GO:006885; P:regulation of pH; IEA.

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Hypothetical protein; Complete proteome.
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Acyl-CoA desaturase (Fragment)
Mamestra brassicae.
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Matches 8; Conservative
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  254 Libisitin 262
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  SEQUENCE FROM N.A.
  NCBI_TaxID=210;
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  OBMZY6
   RESULT 11
  28MZY6
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   DATE OF THE PRINCE OF THE PRIN
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  01-007,

01-007-2002 (TrEMBLrel. 22, Last sequence update)

01-007-2003 (TrEMBLrel. 22, Last sequence update)

01-007-2003 (TrEMBLrel. 25, Last annotation update)

Acyl-0ch desturase (Fragment).

Acyl-0ch desturase (Fragment).

Elodia interpunctella (Indianmeal moth).

Elodia interpunctella (Indianmeal Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;

Nyraldae; Phycitinae; Plodia.
   Spodoptera litura.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea,
Noctuidae, Amphipyrinae, Spodoptera.
NCBL TaxID=69820;
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   STRAIN-ASVQa;
Aripple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
"Evolution of the Integral Membrane Desaturase Gene Family in Moths
and Flies.";
   ô
  MEMBLY, AF482923; AAM28498.1; --
R GO; GO:0005783; C:endoplasmic reticulum; IEA.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
GO; GO:0005200; C:membrane; IEA.
GO; GO:0016491; F:irom ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006633; F:stearoyl-CoA 9-desaturase activity; IEA.
R GO; GO:0006633; P:fatty acid biosynthesis; IEA.
InterPro; IPR05804; FA desaturase.
R InterPro; IPR05804; FA desaturase.
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85.0%; Score 34; DB 5; Length 182;
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182 182
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   Local Similarity 87.5 les 7; Conservative
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  PRELIMINARY;
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   14 LPLOILLM 21
   2 LPLQILLL 9
   2 LPLQILLL 9
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14 LPLQILLM 21

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RESULT 15

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  A Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
A Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
Thipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
The second of the Integral Membrane Desaturase Gene Family in Moths
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The second of the Integral Membrane Gene Family in Moths
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   STRAINENEYS, Rosenfield C.L., You K.M., Jeong S.E.;

"Brolution of the Integral Membrane Desaturase Gene Family in Moths and Flies."

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

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GO, GO:0005703; C:endoplasmic reticulum; IEA.

GO; GO:0005703; C:endoplasmic reticulum; IEA.

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GO; GO:0005703; F:izon ion binding; IEA.

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GO; GO:0004768; F:izon ion binding; IEA.

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InterPro; IPR001822; Desaturase.

InterPro; IPR001804; FA desat_fam.

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FNOW_TER 182

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Last annotation update)
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01-0CT-2002 (TEMBLE). 22, Last seq
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NON TER
SEQUENCE
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Gaps

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2 LPLOILLL 9

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MEDLINE-22705201; PubMed=12810954;
MEDLINE-22705201; PubMed=12810954;
MEDLINE-22705201; PubMed=12810954;
MEDLINE-22705201; PubMed=12810954;
MEDLINE-22705201; Medre E., Reroter A., Holland B., Shen Z., Weber J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus.",
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
BRIEL, AE017146; AAP77474.1; -
SEQUENCE 242 AA; 28014 MW; 5108E98D41244093 CRC64;
   Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
WCBI_TaxID=32025;
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Last annotation update)
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PRT;
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Best Local Similarity 66.7
Matches 6; Conservative
PRELIMINARY;
  1 LIPPOILLE 9
                                 01-OCT-2003 (
01-OCT-2003 (
01-OCT-2003 (
 Q7VHT6
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considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligomucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
   Sequence 9 AA;
  Query Match
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   Human str
Novel hum
Human NOV
Human NOV
Human str
Human SCC
Human SCC
Amino aci
Protein d
Protein d
Human str
Human str
Human pol
Protein e
Murine Cl
Human str
Human 
  Rat CRTI.
Plant yie
   Aae08241 Human s
Abg23378 Novel h
Ada05736 Human N
Ada05732 Human N
Aar67888 Human s
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  March 1, 2004, 17:16:55 ; Search time 45.5556 Seconds (without alignments) 55.820 Million cell updates/sec
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Aau82740 A
Abu07410 A
Abr08471 E
Adb80484 C
Aae08238 A
Aac12472 E
Abd1728 A
Abd1728 A
Abd18330 A
Aae08240 A
Aae08247 A
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  1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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11. geneseqp1980s:*

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3. geneseqp2000s:*

4. geneseqp2001s:*

5. geneseqp2003as:*

6. geneseqp2003as:*
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length: 2000000000
  US-09-905-083-36
  ä
  1 SLLLPLQIL 9
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394
804
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   inimum DB
aximum DB
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| Aab38062 Fragment Aam79694 Human pro Abg13602 Novel hum Abg12769 Novel hum Abg5858 Human gas Abr63586 Human gas Abr63628 Human gas Abb6362 Human gas Abb6368 Fragment Abr71026 Drosophil Abr41229 Human pro Abr3068 Fragment Aab4037 Human DRO Aay99438 Human DRO Aay99438 Human PRO Aay99438 Human PRO Aay99438 Human PRO Aay99438 Human PRO Aay61867 Novel hum Abo44533 Human sec Abo33680 Novel hum Add708633 Human sec Add70863 Human sec | IENTS      |                             |           |           | enzyme peptide #6 (residues 4-12). | SCCE; cytostatic; vaccine; tumour;<br>; prostate; carcinoma; human;<br>asia. |         |             |           |                |           |            |          |           | g stratum corneum chymotrypsin |           | losing cancer especially ovarian cancer, by chymotrypsin enzyme (SCCE). Proteases are art of tumour growth and metastasis, and |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------|-----------|-----------|------------------------------------|------------------------------------------------------------------------------|---------|-------------|-----------|----------------|-----------|------------|----------|-----------|--------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------|
| AAB38062<br>AAM79694<br>ABM12769<br>ABG12769<br>AAB63580<br>AAB63580<br>AAB63580<br>AAB63580<br>AAB71229<br>AAB71229<br>AAB71229<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129<br>AAB7129                                                                                                                                                                                                           | ALIGNMENTS | 9 AA.                       |           |           | chymotrypsin er                    | enzyme;<br>colon<br>nyperpl                                                  |         |             |           |                |           |            |          |           | detecting                      | English.  | diagnosing<br>neum chymot<br>ral part of                                                                                       |
| W444404440WWW40L/L/L                                                                                                                                                                                                                                                                                                                                                                                                                          |            |                             |           | ٤)        | ymot                               | rypsin e<br>t, lung;<br>ignant h                                             |         |             |           | 3977           | 2600      |            |          |           |                                |           | dia<br>orneu                                                                                                                   |
| 40000440000014444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                        |            | ; peptide                   |           | st entry) | corneum ch                         | hymotry<br>breast;<br>; malig                                                |         |             |           | 2001WO-US00397 | US-00502  | ARKANSAS.  |          | . 26.     | comprises                      | 3; 127pp; | relates to diagn<br>stratum corneum<br>be an integral p                                                                        |
| ######################################                                                                                                                                                                                                                                                                                                                                                                                                        |            | standard;                   |           | 1 (first  |                                    | corneum ch<br>ovarian; b<br>e therapy;                                       | ens.    | 8-A1.       |           |                | 0; 2000US | UNIV ARKA  |          | -514676/5 | cancer                         | Page 103  | for                                                                                                                            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                               |            | 41                          | 08241;    | -NOV-2001 | an stratum                         | Stratum co<br>cancer; ov<br>antisense                                        | sapi    | WO200159158 | 6-AUG-200 | -FEB-2001      | -FEB-2000 | (UYAR-) UN | rien TJ  | 2001      | Diagnosing<br>enzyme.          | aim 25;   | The invention<br>screening for<br>considered to                                                                                |
| ろろの2333333333344444 ·<br>る7890123450789012345                                                                                                                                                                                                                                                                                                                                                                                                 |            | RESULT 1 AAE08241 ID AAE082 | AC AAE082 | 01        | DE Human                           | KW Str<br>KW can<br>KW ant                                                   | OS Homo | -           | H         | 0.7            | 11        |            | PI 0'bri | DR WPI;   |                                | ប         | -                                                                                                                              |

o, Length

DB 4;

Score 40;

100.08;

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셤
  The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed carivity of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in adjustical and products format directly from NIPO at the printed specification, but was obtained in the contract of the cont
  ö
   Gaps
   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
   Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging; diagnostic; genetic disorder.
  .
0
   Indels
Pred. No. 1.4e+06;
   Claim 20; SEQ ID NO 53737; 103pp; English
  ftp.wipo.int/pub/published_pct_sequences
   Novel human diagnostic protein #23369.
   ABG23378 standard; protein; 136 AA.
         100.0%; Pr
   Tang YT;
  31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
   30-MAR-2001; 2001WO-US008631
   18-FEB-2002 (first entry)
  Best Local Similarity 100
Matches 9; Conservative
   6 TIOTATTIS
   1 SLLLPLOIL 9
   Drmanac RT, Liu C,
  WPI; 2001-639362/73.
N-PSDB; AAS87565.
  (HYSE-) HYSEQ INC
   Sequence 136 AA;
   WO200175067-A2
   Homo sapiens
  11-OCT-2001
   ABG23378;
  SULT 2
```

Gaps

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h Similarity 100.0%; Score 40; DB 4; Length 136; 9; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 9; Conserv

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Dipippo VA;
   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DM, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee NL, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
   immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
  human, NOVX; antidiabetic; anorectic; antibacterial; virucide;
  ADA05736 standard; protein; 198 AA
   Human NOV18c protein SEQ ID NO:96.
   05-00T-2001; 20010S-0327435P.
05-00T-2001; 20010S-0327449P.
09-00T-2001; 20010S-0327917P.
09-00T-2001; 20010S-0328044P.
09-00T-2001; 20010S-0328056P.
15-00T-2001; 20010S-0328448P.
15-00T-2001; 20010S-0328448P.
  18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349515P.
01-NOV-2001; 2001US-0346357P.
  17-WAY-2002; 2002US-0381642P.
28-WAY-2002; 2002US-0383656P.
29-WAY-2002; 2002US-0383831P.
  2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
  2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
  2002US-0383831P.
2002US-0391335P.
   2002US-0373826P.
  01-OCT-2002; 2002US-00262511
  02-OCT-2002; 2002WO-US031373
  (first entry)
  CURA-) CURAGEN CORP.
10 SLLLPLQIL 18
   WPI; 2003-381626/36.
N-PSDB; ADA05735.
   WO2003029424-A2
   17-APR-2002;
   19-APR-2002;
  19-APR-2002;
   06-NOV-2003
  Homo sapiens
   10-APR-2003.
```

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

10-APR-2003

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) at the composition described above; in one or more containers, the composition described above; (3) an isolated nucleic acid molecule above polypeptide described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a farsate associated with altered levels of expression of the above a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10.) a method for identifying a potential therapeutic agent for a berrant physiological interactions of the polypeptide; (11) a method of general physiological interactions of the polypeptide; (12) a method of method of a pathology associated with the polypeptide for modulator; or preventing a pathology associated with the above polypeptide; (11) a method of preventing a pathology associated with the above polypeptide; or preventing a pathology associated with the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for reacting and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for reacting a cancer, and can be used in gene therapy. The acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic acid solated with a human disease. The polypeptide or preventive disorders such as diabetes or obesity, inference or the polypeptide present invention.

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Sequence 198 AA;

0; Gaps 100.0%; Score 40; DB 6; Length 198; 100.0%; Pred. No. 8.6; 0; Indels iive 0; Mismatches 0; Indels Local Similarity 100.0 Query Match Matches

. 4 SLLIPLOIL 12 1 SLLLPLQIL 9

ADA05732 standard; protein; 250 AA. ESULT 4 DA05732 

ADA05732;

Human NOV18a protein SEQ ID NO:92.

06-NOV-2003 (first entry)

human; NOVX, antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

Homo sapiens.

```
09-0CT-2001; 2001US-0328044P.

12-0CT-2001; 2001US-0328056P.

15-0CT-2001; 2001US-032844P.

17-0CT-2001; 2001US-0328414P.

17-0CT-2001; 2001US-033042P.

24-0CT-2001; 2001US-033926F.

24-0CT-2001; 2001US-033926F.

24-0CT-2001; 2001US-034957P.

29-0CT-2001; 2001US-034957P.

17-APR-2002; 2002US-0373260P.
  2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
02-OCT-2002; 2002WO-US031373.
  19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
  2001US-0327917P
  25-JUN-2002; 2002US-0391335P.
```

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ont T, W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Herghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05731. 

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
colypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiclogical interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to

Sequence 253 AA;

field.)

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a pathology associated with the polypeptide, (12) a method for modulating the activity of the polypeptide described above, (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, immunondulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NoVX from the present invention.
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## Sequence 250 AA;

```
Query Match 100.0%; Score 40; DB 6; Length 250; Best Local Similarity 100.0%; Pred. No. 11; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## 1 SLLLPLOIL 9

ESULT 5 AR67888 D AAR67888 standard;

AAR67888 standard; protein; 253 AA. AAR67888;

25-MAR-2003 (revised) 09-AUG-1995 (first entry) Human stratum corneum chymotrophic recombinant enzyme (SCCE).

Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.

Homo sapiens.

WO9500651-A1.

20-JUN-1994; 94WO-IB000166

18-JUN-1993; 93DK-00000725

(SYMB-) SYMBICOM AB.

Egelrud T, Hansson L;

WPI; 1995-052088/07. N-PSDB; AAQ81203. Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.

Disclosure; Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, ecc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p5507. (Updated on 25-MAR-2003 to correct PN

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   Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid preptide. Its anino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a buman lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cpds. useful for treating or develop products for the design associated with beta-amyloid peptide, esp. Alzheimer's disease
   New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
                          Gaps
  Gaps
   Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
  ô
                          .<u>,</u>
  Length 253;
2; Length 253;
  0; Indels
                          0; Indels
  Ouery Match
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0;
                           Mismatches
  Human amyloid precursor protein protease.
  Score 40;
Pred. No.
   Little SP;
   ABB84421
ID ABB84421 standard; peptide; 253 AA.
   Claim 1; Page 44-45; 55pp; English
   AAW05383 standard; protein; 253 AA.
                           .
0
   96WO-US004294.
 100.0%;
ilarity 100.0%;
Conservative 0
  95US-00416257.
   (first entry)
   Dixon EP, Johnstone EM,
  (ELIL ) LILLY & CO ELI
  SLLLPLOIL 12
  4 SLLLPLOIL 12
  σ
  1 SLLLPLQIL 9
   WPI; 1996-464694/46.
N-PSDB; AAT39783.
  1 STITTBIOIT
  Query Match
Best Local Similarity
   Sequence 253 AA;
  Homo sapiens
   WO9631122-A1
   02-APR-1996;
  04-APR-1995;
   31-DEC-1996
  10-0CT-1996.
  AAW05383;
   cherapy
                             Matches
   RESULT 7
   ઠે
  셤
   qq
   ਨੇ
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(first entry)

us-09-905-083-36.rag

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Human SCCE protein N-terminal fragment SEQ ID 48.
  WPI; 2002-643380/69
08-NOV-2002
```

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SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
  09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
   08-FEB-2002; 2002WO-IB001300
   Egelrud T, Hansson L;
   (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
   WO200262135-A2
  Homo sapiens
  15-AUG-2002.
```

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Example 6; Page 37; 74pp; English

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a commercial or a harmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an pritaris, acopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. Phe mammal of the invention skin diseases which hyperkeratosis, acathosis, epidermal inflammation, dermal inflammation, dermal inclammation, dermal inclammation of the human stratum corneum chymotryptic enzyme, SCCE transgenic mammals described in the invention

Sequence 253 AA;

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                                   Gaps
                                   .
0
        100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels
Query Match
Best Local Similarity luv...
9; Conservative
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SillPloil 12

RESULT 8 ABB84406

ABB84406 standard; protein; 253 AA

ABB84406;

(first entry) 08-NOV-2002

Human SCCE protein.

SCCE, human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal, skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens.

WO200262135-A2.

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218. 

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

ä T, Hansson Sgelrud

WPI; 2002-643380/69. N-PSDB; ABQ76226 Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence compurising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, coperably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or resting of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a composund or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an inflammatory skin diseases selected from diseases consisting of epidermal inflammation, pruritus, acopic dermatitis, eczema, acne and inherited skin diseases in pruritus, acopic dermatitis, eczema, acne and inherited skin diseases prutitus, acopic dermatitis, eczema, acne and inherited skin diseases prutitus, acopic dermatitis, eczema, acne and inherited skin diseases pritch pepidermal phyperkeratosis. The mammal of the intention skin diseases protential composutes of itch mederanisms and the testing of potential compounds and compositions for relieve of various skin diseases potential compounds and compositions for relieve of various skin disease where itch is a component. This sequence represents the human stratum corneum chymotryptic arzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (KLX) and is used in the development of the transgenic mammals described in the invention

Sequence 253 AA;

.. 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels 

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SLLLPLOIL 12 1 SLLLPLQIL 9

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Amino acid sequence of novel human protease #39
AAU82740 standard; protein; 253 AA
   (first entry)
   23-APR-2002
                                       AAU82740;
   Human;
```

protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychoric disorder; neurological disorder; dyskinesia; viral infection; human immundeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.

Homo sapiens.

WO200200860-A2

03-JAN-2002.

26-JUN-2001; 2001WO-US020171.

26-JUN-2000; 2000US-0214047P.

(SUGE-) SUGEN INC

Caenepeel Sudarsanam S, Manning G, Whyte D, Plowman G, W Charydczak G;

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory WPI; 2002-139913/18. N-PSDB; ABK31782.

Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, cioln, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asbhma), cardiovascular diseases (e.g. inflammatory diseases, mitchembosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. districts) or central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention

Sequence 253 AA;

Gaps 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

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1 SLLLPLOIL 9

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4 SLLLPLOIL 12

RESULT 10 ABU07440

ABU07440 standard; protein; 253 AA (first entry) 28-JAN-2003 ABU07440; 

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring. Protein differentially regulated in prostate cancer #43.

Homo sapiens.

WO200281638-A2.

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z, WPI; 2003-058520/05.

N-PSDB; ABX10343.

Novel genes which are differentially regulated in prostate cancer, usel for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of the probability that the sample, where the number is indicative of the probability that the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive contervention in a subject having a prostate cancer. which involves contesting a prostate cancer. Which involves contesting a prostate cancer. Preferably, the expression levels in a sample comprising prostate tissue of target genes which are differentially regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined.

(I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the prostate cancer cells with a test agent under conditions effective for the test agent to modulate such biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its exact of cancer of cancer, in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of eventomer, its atage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus content of the polypeptide encoded by (I) can be used as target for the rapeutic applications to treat prostate of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in disquostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially applications. This is the am regulated in prostate cancer

Sequence 253 AA;

ò

```
The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of traget genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated cancer calls with a test agent under conditions effective for the test agent to modulate a biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, preventing or treating, determining predisposition to diseases and conducts are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer. (I) and its expression products are used encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus
  Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
  Gaps
  Prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
  ö
100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 11; ative 0; Mismatches 0; Indels
   Protein differentially regulated in prostate cancer #74.
   ABU07471 standard; protein; 253 AA.
   Claim 1; Page 351; 416pp; English.
   (ORIG-) ORIGENE TECHNOLOGIES INC.
   06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.
   08-APR-2002; 2002WO-US010824.
  28-JAN-2003 (first entry)
  Conservative
   SLLLPLOIL 12
   1 SELEPEQIE 9
  WPI; 2003-058520/05.
Query Match
Best Local Similarity
Matches 9; Conserv
  N-PSDB; ABX10375
  WO200281638-A2.
  Jay G;
  17-0CT-2002
  ABU07471;
  Sun Z,
   SSULT 11
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   ö
for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways of functionally relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer
   The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
   New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
  Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
  Gaps
   Gaps
   Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
  ô
   ö
  Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 11; Matches 9; Conservative 0; Mismatches 0; Indels
   6; Length 253;
  0; Indels
   100.0%; Score 40; DB 100.0%; Pred. No. 11;
  0; Mismatches
  Claim 2; Page 157-158; 169pp; English.
   ABR58471 standard; protein; 253 AA.
   02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
  02-OCT-2002; 2002WO-US031467.
   (first entry)
  Conservative
  Algate PA, Mannion J;
  4 SLLLPLQIL 12
   4 SLLLPLOIL 12
   1 STILPLOIL 9
  1 SLLLPLQIL 9
   Query Match
Best Local Similarity
Local 9; Conserve
   WPI; 2003-372001/35.
   (CORI-) CORIXA CORP
  Sequence 253 AA;
  Sequence 253 AA;
  WO2003029468-A1.
  Homo sapiens.
   07-JJL-2003
   10-APR-2003.
  ABR58471;
   ABR5847.
           8888888888
```

RESULT 13

(first entry)

04-DEC-2003

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us-09-905-083-36.rag
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The present sequence is human stratum corneum chymotryptic enzyne (HSCEE), a member of the kallikrein multi-gene family. Kallikreins and kallikrein-like protease enzyme kallikrein-like protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L13, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate ancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins
   Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
   New kallikrein-like (XLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
   Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).
   Human; KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6; HSCEE; human stratum corneum chymotryptic enzyme; kallikrein-like protein; serine protease; cytostatic; cancer; prostrate cancer.
  .;
0
   100.0%; Score 40; DB 3; Length 257; 100.0%; Pred. No. 11; tive 0; Mismatches 0; Indels
   Example 4; Fig 17; 184pp; English
   AAE08238 standard; peptide; 9 AA.
  99US-0124260P.
99US-0127386P.
99US-0144919P.
   (MOUN ) MOUNT SINAI HOSPITAL.
   39-MAR-2000; 2000WO-CA000258
   (first entry)
   Yousef GM, Diamandis EP;
   Best Local Similarity 100.
Matches 9; Conservative
  4 SLLIPLOIL 12
  σ
  WPI; 2000-587440/55.
  1 STPLPLOIL
   Sequence 257 AA;
  WO200159158-A1
   WO200053776-A2
  11-MAR-1999;
01-APR-1999;
21-JUL-1999;
   01-NOV-2001
  16-AUG-2001
   14-SEP-2000
   AAE08238;
   Query Match
   RESULT 15
AAE08238
  à
  셤
   ö
  The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a beloogical sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
   Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
  Gaps
   cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
  .
0
   100.0%; Score 40; DB 7; Length 253; 100.0%; Pred. No. 11;
  0; Indels
  0; Mismatches
   Ovarian cancer-associated protein #24
   AAB21326 standard; protein; 257 AA.
  Claim 13; Page 291; 332pp; English.
      )B80484
) ADB80484 standard; protein; 253 AA.
```

(EOSB-) EOS BIOTECHNOLOGY INC

WPI; 2003-167431/16. N-PSDB; ADB80483. Mack DH, Gish KC;

18-JUN-2001, 2001US-0299234P. 27-AUG-2001, 2001US-0315287P. 05-SEP-2001, 2001US-031544P. 13-NOV-2001, 2001US-0350666P. 12-APR-2002, 2002US-0372246P.

18-JUN-2002; 2002WO-US019297

WO2002102235-A2. Homo sapiens

27-DEC-2002.

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Gaps

(first entry)

02-FEB-2001

AAB21326;

RESULT 14 VAB21326

Query Match 100. Best Local Similarity 100. Matches 9; Conservative

Sequence 253 AA;

us-09-905-083-36.rag

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07-FEB-2001; 2001WO-US003977.
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11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 102; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonuclectide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

0; Gaps Query Match 90.0%; Score 36; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 1.46+06; Matches 8; Conservative 0; Mismatches 0; Indels

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1 LLLPLQIL 8

earch completed: March 1, 2004, 17:28:53 ob time : 46.5556 secs

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1 SILLPLOIL 9
   US-09-918-243-36
   US-09-502-600-36
  US-09-502-600-36
  FEATURE:
  ð
   В
   Sequence 116, App
Sequence 10804, A
Sequence 13, Appl
Sequence 5049, Ap
Sequence 593, Appl
Sequence 59, Appl
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 27661, Ap
  Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
  Sequence 33, Appl
Sequence 12075, A
Sequence 35, Appl
  Sequence 36, App]
Sequence 36, App]
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  March 1, 2004, 17:21:46; Search time 11.8889 Seconds (without alignments) 39.081 Million cell updates/sec
  Sequence 3, Ap
Sequence 2, Ap
Sequence 33, A
  Sequence 3,
  Sequence 11
Sequence 35
Sequence 11
   Description
   Sequence 2
Sequence 2
   Sequence
   Issued Patents AA:*

/ cgm2 6/ptodata/2/iaa/5A_COMB.pep:*
// cgm2 6/ptodata/2/iaa/5B_COMB.pep:*
// cgm2 6/ptodata/2/iaa/6A_COMB.pep:*
// cgm2 6/ptodata/2/iaa/6A_COMB.pep:*
// cgm2 6/ptodata/2/iaa/FGTCOMB.pep:*
// cgm2 6/ptodata/2/iaa/PcTUS_COMB.pep:*
// cgm2 6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
   US-09-750-160-64-3
US-09-764-766-3
US-09-764-766-3
US-09-918-243-33
US-09-918-243-33
US-09-918-243-33
US-09-918-243-35
US-09-918-243-116
   US-09-328-352-7861
US-09-252-991A-22663
US-09-252-991A-27921
   US-09-543-681A-5049
US-09-170-496D-293
US-09-364-425B-58
   otal number of hits satisfying chosen parameters:
   389414 segs, 51625971 residues
   SUMMARIES
   ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  M protein - protein search, using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  seq length: 0
seq length: 200000000
  US-09-905-083-36
  1 SLLLPLQIL 9
   Length
  812
  557
181
307
   1000.0
1000.0
1000.0
1000.0
90.0
85.0
   Match
  itle:
erfect score:
equence:
  Score
  coring table:
   linimum DB (laximum DB )
  atabase:
  earched:
   no un
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|                     | Ξ.                   |                 |                      | Sequence 323, App | 57               | Sequence 7, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 24, Appl | 24,              | 22,              | Sequence 40, Appl | Sequence 40, Appl | Sequence 19, Appl | Seguence 6, Appli | \ppl             | Sequence 6227, Ap   |
|---------------------|----------------------|-----------------|----------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|---------------------|
| US-09-489-039A-8947 | US-09-489-039A-11785 | US-08-677-049-6 | US-09-489-039A-10791 | US-09-489-847-323 | US-08-676-279-57 | US-07-777-715-7   | US-08-170-126-2   | US-08-954-418-2   | US-08-753-007A-24 | US-09-398-496-24 | US-08-977-378-22 | US-08-630-172-40  | US-09-375-419-40  | US-08-339-152A-19 | US-08-007-999B-6  | US-08-689-276A-6 | US-09-543-681A-6227 |
| 4                   | 4,                   | N               | 4                    | 4                 | Ŋ                | Н                 | Н                 | m                 | m                 | m                | 4                | m                 | m                 | -                 | N                 | N                | 4                   |
| 404                 | 436                  | 463             | 474                  | 542               | 549              | 1098              | 1098              | 1098              | 21                | 21               | 22               | 26                | 26                | 190               | 190               | 190              | 195                 |
| 0.                  | 0                    | 0               | 0                    | 0                 | 0                | 0.                | 0                 | 0                 | 'n                | ų                | ιū               | 'n                | 'n                | 'n                | 'n                | 'n               | ιú                  |
| 75                  | 75                   | 75              | 75                   | 75                | 75               | 75                | 75                | 75                | 72                | 72.5             | 72               | 72                | 72                | 72                | 72                | 72               | 72                  |
| 30                  | 30                   | 30              | 30                   | 30                | 30               | 30                | 30                | 30                | 29                | 29               | 29               | 29                | 53                | 29                | 6                 | 5                | 29                  |
| 28                  | 29                   | 30              | 31                   | 33                | 1 6              | 34                | 35                | 36                | 37                | 38               | 39               | 40                | 41                | 4                 | . <del>4</del> ,  | 44               | 74                  |

## ALIGNMENTS

```
RESULT 1

US-09-202-60-36

US-09-202-60-36

Sequence 36, Application US/09502600A

REPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

FILE REPRENCE: D623201P-C

CURRENT FILEMED DATE: 200-02-11

CURRENT FILEMED DATE: 200-02-11

PRIOR PILICATION NUMBER: 09/039,211

NUMBER OF SEQ ID NOS: 136

LENGTH; 9

LENGTH; 9

LENGTH; 000-04-11

US-09-502-600-36

COMER INVENTION: Residues 4-12 of the SCCE protein
US-09-502-600-36

LENGTH; 000-04-11

US-09-502-600-36

US-09-102-04-11

SEBULT 2

RESULT 2

RESULT 2

RESULT 3

RESULT 3

RESULT 4

APPLICANT: Ganlon, Markin J.

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

LENGTH; 000-04-11

UTFR: REPERENCE: D6-201-07-13

VIPE: REPERENCE: D6-201-07-13

URBER OF SEQ ID NOS: 136

LENGTH; 000-04-11

US-09-09-005-005-000-04-11

US-09-005-005-000-04-11

US-09-005-005-000-04-11

US-09-005-005-000-04-11

US-09-005-000-04-11

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Sequence 2, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Eqelrid, Torbjorn
APPLICANT: Hanseon, Lennart
ATILE OF INVENTION: Razyme (SCCE)
NUMBER OF SEQUENCES: 1
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Department Policy Compatible
CORRESPONDENCES: Department Policy Compatible
COMPUTER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                             100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 3e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE STEERIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
-09-918-243-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMOUNICATION INFORMATION:
TELECHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                      Query Match
Best Local Similarity 100...
Pest Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SLLLPLOIL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 4
JS-08-824-874-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-08-557-146-2
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US-09-154-344-2
) Sequence 2, Application US/09154344
) Sequence 2, Application US/09154344
) Patent NO. 5981256
GENERAL INFORMATION:
APPLICANT: Bealand, Torbjorn
APPLICANT: Hanson, Lennart
ITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
ITLE OF INVENTION: Bnzyme (SCCE)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELSE FLOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: TWORMATION:
AME: BILLING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                              Palo Alto
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                                                                                                                                        USA
                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                            94304
                                                                                                                                     COUNTRY:
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US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
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              Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                            4 SLLLPLOIL 12
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                                                                                                     1 SLLLPLQIL 9
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LIBRARY: GenBank
CLONE: 532504
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US-09-210-084-3
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APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REFERENCE/OCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: (212) 819-878
TELECAX: (212) 84-8113
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amilio acids
TYPE: amilio acid
TYPE: amilio acid
TYPE: amilio acid
TYPE: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Indiana COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REBERGNOCKOFT NUMBER: x9239
TELECOMMUNICATION INFORMATION:
TELEFAX: 317-27-1090
TELEFAX: 317-27-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08930188
Patent No. 6093397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLCGY: linear
MOLECULE TYPE: protein
JS-08-930-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SLLLPLOIL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLLLPLQIL 9
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                                                                                                                                                                                                                                                                                                                                                                      3-09-154-344-2
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S-08-930-188-2
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0
100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 1.8; tive 0; Mismatches 0; Indels
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100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECHONICATION INFORMATION:
TELECHONE: 415-85-055
TELERBIONE: 415-85-0555
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US 08/416,257
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein PCT-US96-04294-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLLLPLQIL 9
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US-09-502-600-33
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Sequence 2. Application PC/TUS9604294

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Juttle, Sheala P.

TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF ENGUNCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSER: 11111y and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STREET: Grain and States of America
CITY: United States of America
CONDUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PLOSPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PROSPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PLOSPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PROSPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PROSPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PROSPY DISK

COMPUTER READABLE

COMPUTER READ
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                                                                                                                                                                                                                                                                                                             MEDIUM ITE: IDEACULE
COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION ATONER: 09/210,084
FILING DATE: CURROWN>
APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: CURROWN>
APPLICATION NUMBER: 97-49
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0252 US
TELEFORMUNICATION INFORMATION:
TELEFORM 415-845-4166
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: 512504
SEQUENCE DESCRIPTION: SEQ ID NO: 3: S-09-764-762-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 253 amino acids
                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
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                                                                                                                                              STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLLLPLQIL 9
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CT-US96-04294-2
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Patent No. 6294344

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Overtien Cancer
FILE REFERENCE: D6223GTP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR PAPPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1996
NUMBER OF SEQ ID NOS: 136

EENGTH: 9

LENGTH: 9
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Patent No. 6627403

GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REPERENCE: D6223CIP/C/P/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30

PRICR APPLICATION NUMBER: US
PRICR FILING DATE: 2001-07-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 36; DB 3; Length 9; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapiens PETURE: PRTURE: PRTURE: PRTURE: COTHER INCOMMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: 38,082
REFERENCE/DOCKET NUMBER: 38,082
TELECOMMUNICATION INFORMATION:
TELEFAM: 317-27-1090
TENGTH: 253 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
```

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Sequence 35, Application US/09918243
; Sequence 35, Application US/09918243
; Patent No. 6627403
; GRERAL INFORMATION:
    APPLICANT: O'Brien, Timothy J.
    APPLICANT: Santin, Martin J.
    APPLICANT: Santin, Alessandro
    TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE OF INVENTION: METHOD FOR CURRENT TILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
    PRIOR PLICATION NUMBER: US
    PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
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OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-918-243-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-502-600-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 32; DB 4;
100.0%; Pred. No. 3e+05;
tive 0; Mismatches
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                                                                                                                            US-09-502-600-116
Sequence 116, Application US/09502600A
; Patent No. 6294344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLLLPLO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLLPLQ 9
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                                          1 LLPLOIL
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US-09-918-243-35
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Sequence 12075, Application US/09489039A
Patent No. 6610336
Patent No. 661036
Patent No. 661036
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PREMOMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PAPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PRIOR DATE: 1999-01-29
NUMBER 0F SEQ ID NOS: 14342
SEQ ID NO 12075
LENGTH: 912
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Patent No. 6294344

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Overlan Cancer

TITLE OF INVENTION: Overlan Cancer

FILE REFERENCE: D6222CIP-C

CURRENT FILING DATE: 2000-02-11

CURRENT FILING DATE: 2000-02-11

CURRENT FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35

LENGTH: 9
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Pred. No. 94;
1; Mismatches 0; Indels
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80.0%; Score 32; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                90.0%; Score 36; DB 4; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
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; OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-35
                                                                                                                   NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
1S-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Klebsiella pneumoniae
JS-09-489-039A-12075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
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ORGANISM: Homo sapiens
                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-502-600-35
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                                                                                                    FEATURE
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Sequence 36, Application US/09905083; Patent No. US20020146708A1; GENERAL INFORMATION:
9; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-905-083-36
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Sequence 38, Appl
Sequence 38, Appl
Sequence 90, Appl
Sequence 498, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 13, Appl
Sequence 116, Appl
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                                                                March 1, 2004, 17:35:01 ; Search time 24:1111 Seconds (without alignments) 78.818 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/PCT_MBW_PUBL.pep:*

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17: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpaa/USO6_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/USO6_PUBCOMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-083-36
US-09-905-083-36
US-09-764-762-3
US-09-764-762-3
4 US-10-264-283-90
5 US-10-13-999-48
US-09-905-083-33
US-10-13-999-48
US-09-905-083-33
US-10-13-999-48
US-09-905-083-35
US-10-216-055A-28
US-09-918-243-315
US-09-918-243-315
US-09-918-243-315
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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3867, Ap
148, App
1081, App
11081, App
1131, App
1131, App
1131, App
1131, App
1131, App
1138, App
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                                 Sequence Seq
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Sequence 3
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; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36
US-10-104-047-3867

US-10-302-267-148

US-10-374-7804-2272

US-10-156-761-10881

US-10-056-882-135

US-10-056-882-135

US-10-006-8184-338

US-10-006-8184-338

US-10-015-3934-338

US-10-015-3934-338

US-10-015-1214-338

US-10-017-1214-338

US-10-017-5274-338

US-10-017-5274-338

US-10-017-5274-338

US-10-017-5274-338

US-10-017-5274-338

US-10-017-5274-338

US-10-017-5384-338

US-10-017-5384-338

US-10-017-5384-338

US-10-017-5384-338

US-10-017-5384-338

US-10-017-5384-338

US-10-017-61834-338

US-10-017-61834-338

US-10-017-61834-338

US-10-017-61834-338

US-10-018-3484-338

US-10-018-3484-338

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US-10-018-3484-338

US-10-018-3484-338
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CITY: Palo Alto

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4 SLLLPLOIL 12
                                                     COUNTRY: USA
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian cancer
FITLE OF INVENTION: Ovarian cancer
FILE REFERENCE: D6223GIP/C/Dia
CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR PILING DATE: 2000-02-11
SEQ ID NO 36
LENGTH: 9
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                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
S-09-905-083-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
SADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Setent No. US2020064856A1
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CARNEDEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
APPLICANTION: NOVEL PROTEASES
FILE REFERENCE: 036602/121
CURRENT FILING DATE: 2001-06-26
RADOR APPLICATION NUMBER: 60/214,047
PRIOR PRILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09764762
Patent No. US20020068341A1
GENERAL INFORMATION:
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
IS-09-888-615-98
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ORGANISM: Homo sapiens
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Sequence 90, Application US/10264283

Publication No. US20030144494A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INFORMATION: COMPOSITIONS AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.590 IAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.590 IAGNOSIS OF OVARIAN CANCER
CURRENT PAPLICATION NUMBER: US/10/264,283

CURRENT PAPLICATION DAYS: 111

SOFTWARE COFIXE INVENTION DISCIOSURE Database

SOFTWARE COFIXE INVENTION DISCIOSURE DATAB
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: IBM Compatible
CURRENTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
FULNG DATE: IB-Jan-2001
CLASSIFICATION NUMBER: US/09/764,762
FILING DATE: IB-Jan-2001
CLASSIFICATION NUMBER: 09/210,084
FILING DATE: CURKNOWN:
APPLICATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/MATION NUMBER: 36,749
REFERENCE CHARACTERISTICS:
LENGTH: 253 amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
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Best Local Similarity 100.
Matches 9, Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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2 LLLPLQIL
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US-09-918-243-33
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                                                                                                                                                                                                         APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kutt C.
APPLICANT: Gish, Kutt C.
APPLICANT: Hevezl, Peter A.
APPLICANT: Hevezl, Peter A.
APPLICANT: Hevezl, Peter A.
APPLICANT: Box Biotechnology, Inc.
APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Mathods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 002-11-13
PRIOR APPLICATION NUMBER: US 00/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-10-3
PRIOR PILING DATE: 2001-10-3
PRIOR PILING DATE: 2001-01-3
PRIOR PILING DATE: 2001-01-3
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-03
PRI
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Sequence 48, Application US/1017399
Sequence 48, Application US/1017399
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt G.
APPLICANT: Gish, Kurt G.
TITLE OF INVENTION: Methods of Diagnosis of Cvarian Cancer, Compositions
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002420US
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
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100.0%; Score 40; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0
                         Sequence 498, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Perer A.
APPLICANT: Hevezi, Perer A.
APPLICANT: Mack, David H.
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JS-10-295-027-498
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5-10-295-027-498
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Sequence 33, Application US/09918243

Sequence 33, Application US/09918243

Sequence 33, Application US/09918243

APPLICANT: O'Brien, Timothy J.

APPLICANT: Santin, Jessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6222CIP/C/D/CIP

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 33

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33
                                                                                                                                                                                                                                                                                                                     Mismatches
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-08-27
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 48
LENGTH: 253
                                                                                                                                                                                                                                                                                100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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CRGANISM: Homo sapiens
US-10-173-999-48
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RESULT 13
US-09-918-243-116
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Sequence 10255, Application US/10369493
Publication No. US20030233675A1
Publication No. US20030233675A1
Sequence 10255, Application US/10369493
Publication No. US20030233675A1
APPLICANT: Cao, Yongwei
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Serven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXARESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXARESSION US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10255
LENGTH: 868
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88.9%; Pred. No. 3.8e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          Query Match

90.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels
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Publication No. US20030134328A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GOTTON:
GOTTON:
GOTTON:
GOTTON:
APPLICANT:
MATTER OF THE REPRESS:
APPLICANT:
MATTER OF INVENTION:
MARKALLAN GENES; RELATED REAGENTS
FILE REPRESENCE:
TILLE OF INVENTION:
MARKALLAN GENES; RELATED REAGENTS
FILE REPRESENCE:
TILLE OF INVENTION:
MARKALLAN GENES; RELATED REAGENTS
FILE REPRESENCE:
TOTAL OF INVENTION:
MARKALLAN GENES; RELATED REAGENTS
FILE REPRESENCE:
TOTAL OF INVENTION NUMBER:
US/10/236,055A
CURRENT APPLICATION NUMBER:
US/10/236,055A
CURRENT APPLICATION NUMBER:
US/10/236,055A
CURRENT APPLICATION NUMBER:
SOSTWARE ENTER ENTER TOTAL OF THE SOST OF 
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHÁIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein 5-09-905-083-33
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Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Mus musculus
IS-10-236-055A-28
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Sequence 116, Application US/09918243

Sequence 116, Application US/09918243

SETION OF SETION: O'BRIGHT O'S TIME OF O'S TIME 
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; Sequence 35, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
    APPLICANT: O'Brien, Timothy J.
    APPLICANT: Santin, Alesandro
    TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223CIP/C/D/CIP
    CURRENT APPLICATION NUMBER: US/09/918,243
    CURRENT APPLICATION NUMBER: US
    PRIOR PILING DATE: 2001-07-30
    PRIOR PILING DATE: 2001-07-13
    NUMBER OF SEQ ID NOS: 136
    LENGTH: 9
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Score 33; DB 14; Length 804;
Pred. No. 8e+02;
2; Mismatches 0; Indels
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, OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-918-243-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-918-243-35
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Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0;
         Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative 2
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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3 SLLLPLO 9

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JS-09-905-083-35
Sequence 35, Application US/09905083
Sequence 35, Application US/09905083
Sequence 35, Application US/09905083
Patent No. US20020146708A1
SEQUENCE TO SET TIME OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: OVATIAN CAMPOSITION: OVATIAN CAMPOSITION: OVATIAN CAMPOSITION: OVATIAN CAMPOSITION: OVATIAN CAMPOSITION: OVATIAN APPLICATION WUMBER: US/09/905,083
CURRENT FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
LENGTH: 9
THE TOTAL OF THE TOTAL OVATIAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Sequence 116, Application US/09905083
Sequence 116, Application US/09905083
Sequence 116, Application Sequence 116, Applications of Sequence 116, Applications Conserved Sequence 116, Application Concer FILE REFERENCE: D6223CIP/C/Div CURRENT Application NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
LENGTH: 9
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80.0%; Score 32; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 7; Conservative 0; Mismatches 0; Indels
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NAME/KEY: CHAIN
1 NAME/KEY: CHAIN
2 OTHER INCRMATION: Residues 2-10 of the SCCE protein
US-09-905-083-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAMBKEY: CHAIN
NAMBKEY: CHAIN
1019-905-083-35
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Search completed: March 1, 2004, 18:08:52 Job time : 25.1111 secs

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                                                         1, 2004, 17:21:01 ; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                          283366 segs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
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JC7300
JC4857
B85327
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B95976
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interleukin-2 prec interleukin-2 prec probable membrane	hypothetical prote probable phosphate NADH2 dehydrogenas	hypothetical prote cell division prot cytochrome aa3 con	probable high affi T-cell surface gly conserved hypothet	surfactant protein conglutinin precur conglutinin - bovi	probable transport
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## ALIGNMENTS

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serior proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J; Balol. Chem: 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym:
A;Reference number: A53668, MuID:94308255; PMID:8034709
A;Accession: A3368
A;Accession
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Pred. No. 1.5;
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A,Cross-references: GDB:377730
A,Map position: 7435-7435
C,Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology
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RESULT 2

C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 08-Sep-2000 hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

Cyaccession: H7201 Cyaccession: H7201 Ryanonymous, Genoscope Submitted to the EMBL Data Library, July 1999 A, Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struk A, Rocession: H75201 A, Status: preliminary A, Rolecule : 1ype: DA A, Rolecule : Lype: DA A, Residues: 1-146 < RAW> A, Residues: 1-146 < RAW> A, Residues: 1-146 < RAW> A, Experimental source: strain Orsay

C.Genetics: A.Gene: PABO088 C.Superfamily: Pyrococcus abyssi hypothetical protein PABO088

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R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                         1-acyl-sn-glycerol-3-phosphate acyltransferase plsC [imported] - Agrobacterium tumefacier
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AC2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58, C.Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: C97402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: AC2620
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <KUR>
A;Residues: GB:AE08688; PIDN:AAL41377.1; PID:g17738693; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: GB: AE007869; PIDN: AAK86172.1; PID: 915155265; GSPDB: GN00169
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                            80.0%; Score 32; DB 2; Length 218; 100.0%; Pred. No. 52; ive 0; Mismatches 0; Indels
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80.0%; Score 32; DB
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches
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ilarity 75.0%; Pred. No. 64;
Conservative 2; Mismatches
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A;Map position: circular chromosome
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                                                  Similarity 100.
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19 ILLPLQLL 26
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A;Molecule type: DNA
A;Residues: 1-264 <KUR>
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DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
roc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map position: 4
Note: 11338.20
Note: intron positions not resolved
Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homolo
Keywords: transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Alternate names: protein T13/8.220
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
;Paccession: T02912; T51654

"Accession: T02912; T51654

"Ubmitted to the Protein Sequence Database, February 1999
;Reference number: Z14766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paz-Ares, J.; Weisshaar, B.
Jant J. 16, 253-276, 1998
J.Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
Reference number: Z14349; MUID:9839469; PMID:9839469
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bate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               robable transcription factor MYB41 [similarity] - Arabidopsis thaliana (fragment)
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Molecule type: DNA
;Residues: 1370 <400.
;Cross-references: GB:AE008917; PIDN:AAL51837.1; PID:g17982584; GSPDB:GN00190
;Experimental source: strain 16M
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75.0%; Pred. No. 57;
ive 2; Mismatches 0; Indels
        DB 2; Length 146;
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Experimental source: cultivar Columbia
     Score 38; DB;
Pred. No. 2.2;
1; Mismatches
        95.0%;
88.9%;
Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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293 ILLPLQVL 300
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66 SLLLPLOII 74
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Residues: 1-218 < KRA>
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A,Gene: AT4g28110
A,Map position: 4
C,Superfamily: barley myb-related protein 3; myb DNA-binding repeat homology
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Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0
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                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                              168 SLLLPLO 174
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                                                                                                                                                                                                                                  1 SLLLPLO 7
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                                                                                                                     Query Match
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      ax-responsive element-binding protein 5 - mouse
Species: Mus musculus (house mouse)
Species: Mus musculus (house mouse)
Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
Maccession: JC7300
Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
Masaki, T.; 187-193, 2000
JTile: Isolation and characterization of the gene encoding mouse tax-responsive elemen Reference number: JC7300
Molecula type: mRNA
Residues: 1-266 <MAS>
Constitues: 1-266 <MAS>
Constitues: 1-266 <MAS>
Constitues: 1-266 <MAS>
Constitues: 1-266 <MAS>
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Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.

Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.

Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.

Kochem. Biophys. Res. Commun. 224, 746-751, 1996

; Reference number: JC4857
; Recession: JC4857
; Molecule type: mRNA
; Residues: 1-267 cKIS>
; Comment: This is a basic-leucine zipper type transcription factor involved in hepatoce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               robable transcription factor MYB41 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001 Accession: B85327 (Species: Arabidopsis Genome Sequencing Consortium, The Cold Springiume 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.;Reference number: A85001; MUID:20083488; PMID:10617198
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,Modecule type: DNA
,Residues: 1-282 SATO
;Cross-references: GB:NC_001268; NID:g7269665; PIDN:CAB79613.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                    ;Gene: treb5
;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
;Keywords: leucine zipper; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: X box-binding protein 1, fos/jun DNA-binding domain homology Keywords: leucine zipper; transcription factor 58-98/Domain: fos/jun DNA-binding domain homology <FJD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: Rattus norvegicus (Norway rat)
;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 08-Sep-1997
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100.0%; Pred. No. 64;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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probable transport protein, similar to Wzx exoT [imported] - Sinorhizobium meliloti (Str. C'Species: Sinorhizobium meliloti (Species: Species: Species
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R;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J;Bacteriol. 175, 7045-7055, 1993
B;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J;Bacteriol. 175, 7045-7055, 1993
A;Title: Genes needed for the modification, polymerization, export, and processing of a;Feference number: A49349; MUID:94042870; PMID:8226646
A;Reference number: A49349
A;Reference number: A49349
A;Reference type: DNA
A;Residues: 1-494 cdLD.
A;Residues: 1-494 cdLD.
A;Residues: 1-494 cdLD.
A;Cross-references: GB:L20758; NID:9393240; PIDN:AAA16050.1; PID:9393249
C;Superfamily: hypothetical protein
C;Keywords: transmembrane protein
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-2000
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80.0%; Score 32; DB 2; Length 282; 100.0%; Pred. No. 68; 0; Indels ive 0; Indels
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80.0%; Score 32; DB 2; Length 494;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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C;Species: Escherichia coli comentation coll (C;Date: 12-Sep-1997 #Sext. Change 01-Mar-2002 C;Accession: G65039 #Sequence_revision 17-Sep-1997 #Sext. Change 01-Mar-2002 C;Accession: G65039 #Sequence Fili, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MuID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pypothetical protein At2947360 [imported] - Arabidopsis thaliana
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cipacesion: C84914
Eilin, X.: Kaul, S.; Rounsley, S.D.; Shaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shan, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Asture 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AE000347, GB:U00096, NID:g2367142, PIDN:AAC75661.1, PID:g1788965, A,Experimental source: strain K-12, substrain MG1655
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A;Residues: 1-196 <BLAT>
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hypothetical protein b2612 - Escherichia coli (strain K-12)
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Pred. No. 1.2e+02;
0; Mismatches 2.
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77.8%;
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-303 <STO>
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C84914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  robable membrane protein YOR137c - yeast (Saccharomyces cerevisiae)
Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
Alternate names: hypothetical protein 0329; hypothetical protein YOR3329c
Alternate Saccharomyces cerevisiae
Accession: S61692; S67022
Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia ubmitted to the EMBL Data Library, December 1995
Accession: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome Reference number: S61643
                                                                                                                                                                                                                                                                                                                                                                                                                         Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A. ubmitted to the EMBL Data Library, April 1993 .;Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT and exoI
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Residues: 1-622 <VOS>
Crose-references: FNBL:Z75045; NID:g1420348; PID:e252028; PID:g1420349; MIPS:YOR137c
Experimental source: strain S288C
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;Residues: 1-622 <BMB:X94335; NID:g1262139; PID:e217839; PID:g1164980
;Corosa-references: EMBL:X94335; NID:g1262139; PID:e217839; PID:g1164980
;Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W.
ubmitted to the Protein Sequence Database, July 1996
*Reference number: S66965
;Accession: S67022
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                                                                                                                                                                                                                                                                                  xoT protein - Rhizobium meliloti
;Species: Rhizobium meliloti
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
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80.0%; Score 32; DB 2; Length 582;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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Cross-references: EMBL: Z22646;Superfamily: hypothetical protein b2046

Reference number: S40173

Accession: S40176

Accession: S40176;Status: preliminary;Molecule type: DNA;Residues: 1-582 <BEC>

|||:|||: 122 SLLIPLOL 129

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Best Loc Matches

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80.0%; Score 32; DB 2; Length 622; 66.7%; Pred. No. 1.5e+02; tive 2; Mismatches 1; Indels

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Best Loc Matches

Query Match

141 SALIPLOVL 149

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ESULT 14 65039

1 SLLLPLOIL 9

Keywords: transmembrane protein 11-27/Domain: transmembrane #status predicted <TMM>

Cross-references: SGD:S0005663

Accession: S61692

us-09-905-083-36.rsp

neisseria m neisseria m drosophila

odontella s

homo sapien

phodopus su homo sapien

canis famil agrobacteri

P30433 Q9pie4 O21515 P01732 P33706 Q04342 Q00825 Q00825 Q00326 Q9jtx5

pongo pygma campylobact

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Hansson L., Stroemgvist M., Baeckman A., Wallbrandt P., Carlstein A., Bgelrud T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chymotryptic enzyme.",
Biochem. Biophys. Res. Commun. 211:586-589(1995).
Procrion: May catalyze the degradation of intercellular cohesive structures in the cornfited layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skytt A., Stroemgyist M., Egelrud T., "Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                         (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yousef G.M., Scorilas A., Diamandis E.P.; Molecular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene.", submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T., "Epidermal overexpression of stratum corneum chymotryptic enzyme mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                 253 AA
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MEDLINE=95314630; PubMed=7794273;
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KLK7 OR PRSSG OR SCCE.
HOMO Sapiens (Human).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-1-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammarory cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.
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Q9DIM7; Q9CRE4;
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
FKSO6 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FKSO6-binding protein)
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REMBL; AF243527; AAG33460.1;

REMBL; AF3968; A53968.

R PRIS, A53968; A53968.

R HSSP; P007631 1DPO.

R MEROPS; S01.300; -...

R GG; GO:0008236; F:serine-type peptidase activity; TAS.

R GO; GO:000824; P:epidermal differentiation; TAS.

R GO; GO:000854; P:epidermal differentiation; TAS.

R GO; GO:000854; P:epidermal differentiation; TAS.

R InterPro; IPRO10214; Peptidase_31.

InterPro; IPRO11314; Peptidase_31.

R PROSTIE; PS00022; TYPP SPS.

R PROSTIE; PS00134; TRYPSIN DOM; 1.

R PROSTIE; PS00134; TRYPSIN DOM; 1.

R PROSTIE; PS00134; TRYPSIN DOM; 1.

R PROSTIE; PS00134; TRYPSIN BRR; 1.

R PROSTIE; PS00134; TRYPSIN BRR; 1.

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CEMENTOGE, WELTERED CONTIGUES, Controlled, Northbridge, Muringe, Mus. Mommalian, Euthbridge, Rodentia; Sciurognathi, Muridae, Murinae, Mus. Mus. This Euthbridge, Trisurae A. Fikhurashi, V. Koshino M. Itoh M., Itoh M., Itohi, Y., Azakawa M., Manina, M. K. Kiyosama H., Kondo, S., Yammanka I., Sharawa K., Itawa M., Mishia K., Kiyosama H., Kondo, S., Yammanka I., Sharawa K., Itawa M., Mishia M., K. Kiyosama H., Kondo, S., Yammanka I., Sharawa K., Itawa M., Mishia M., Mono H., Saldarahi R., Odazakubuni Y., Azakawa K., Itawa M., Mishia M., Mono H., Baldarahi R., Odazakubuni Y., Manina M., Mani
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=92829;
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Q8PLY8;
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YG47 XANAC
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             DRANGO BARANGO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vulpecula).";

J. Mol. Endocrinol. 21:141-152(1998)

-1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULARTING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GRAN CELL DEVELOPMENT AND MATURATION,
REXTHROLD DIFFERENTIATION, INSULIN SECRETION, REVENT CELL SURVITAL
EMBRYONIC AXIAL DEVELOPERAT OR BONE GROWTH, DEPENDING ON THEIR SUBJUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99027340; PubMed=9801457;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Varmontfort D.J., McNatty K.;
"CDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
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                                                                                                                          FK506 BINDING PROTEIN 11.
PPIASE, FKBP-TYPE
5 -> F (IN REF. 1; BAB31559).
5 -> R (IN REF. 1; BAB31559).
94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                         Query Match 85.0%; Score 34; DB 1; Length 201; Best Local Similarity 87.5%; Pred. No. 8.3; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF033340; AAC63945.1; -. 600 Go.0005576; C:extracellular; ISS. GO. GO.0005576; C:extracellular; ISS. GO. GO.0017106; F:activin inhibitor activity; ISS. GO. GO.0003125; F:cytokine activity; ISS. GO. GO.0003739; F:defense/fimmulity protein activity; ISS. GO. GO.0008013; F:growth factor activity; ISS. GO. GO.0005129; F:hormone activity; ISS. GO. GO.0005129; F:hormone activity; ISS. GO. GO.000515; F:protein binding; ISS. GO. GO.0007050; P:cell cycle arrest; ISS. GO. GO.00070519; F:cell differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B. SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
Inhibin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AA
PROSITE; PS00454; FKBP PPIASE 2; FALSE_NEG. PROSITE; PS50059; FKBP PPIASE_3; 1. Isomerase; Rotamase; Signal. 27 GNAL 28 201 PK506 BINDING
                                                                                                                             28 201 FK
57 144 PP
53 53 53
198 198 S
201 AA; 22137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLLPLOLL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IHA TRIVU
077755;
                                                                                                                                                            DOMAIN
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
THA_TRIVU
      RESEPTEED
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GO; GO:0008151; P:cell growth and/or maintenance; ISS.
GO; GO:0007565; P:cell surface receptor linked signal transdu. .; ISS.
BR GO; GO:0007267; P:cell-cell signaling; ISS.
BR GO; GO:0007267; P:cell-cell signaling; ISS.
BR GO; GO:000517; P:hemoglobin biosynthesis; ISS.
BR GO; GO:004578; P:hemoglobin biosynthesis; ISS.
BR GO; GO:0045078; P:hegative regulation of follicle-stimulating. .; ISS.
BR GO; GO:004507; P:hegative regulation of interferor-gamma bio. .; ISS.
BR GO; GO:004226; P:hegative regulation of phosphorylation; ISS.
BR GO; GO:004399; P:heurogenesis; ISS.
BR GO; GO:0046881; P:posttive regulation of phosphorylation; ISS.
BR GO; GO:0046881; P:posttive regulation of follicle-stimulating. .; ISS.
BR GO; GO:0046881; P:posttive regulation of follicle-stimulating. .; ISS.
BR THEFPO; IPRO0189; TGFb.
BR PRINTS; PRO0669; INHIBINA.
BR PROSITE; PRO0187; TGFBIA. 1; 1.
BR PROSITE; PRODEF; IPPOPETIAL.
BR SWART; SMO0204; TGFBIA. 1; 1.
BR SWART; SMO0204; TGFBIA. 1; 1.
BR SIMILARILY.
SIGNAL IPPOPEP STORES INTLARILY.
SIGNAL IPPOPEP STORES INTLARILY.
SIGNAL IPPOPEP STORES INTLARILY.
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SEQUENCE FROM N.A.

CLAIN=306 / ATCC 11902 / XV 101;

MEDLINE=2202145; Pubmde=12024217;

Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A lose L.M.C., A Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Rais J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Raisuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins E.C., Madanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins E.C., Machado M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
INHIBIN ALPHA CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 361;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38945 MW; D661CDF93CDAA87D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein XAC1647.
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us-09-905-083-36.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

C. STRAIN=C57BL/6J; TISSUE=Head;

X. MEDLINE=22346681;

A. VILL OSATON, Saito R., Suzuki H., Yamanaka I., Khodo S.,

A. Visaik Y., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gdjobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Teme D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Chothia C., Golbori T.,

Baldarelli R., Fletcher C.E., Forrest A., Faraer K.S.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Grimmond S., Gduefindich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M. King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

A Majlott D.R., Maltais L., Marchionni L., McKenie L., Mkii H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Persole G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

A Ravasi T., Reed J.C., Reed D.J., Reid C., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Wilming L.G., Wanlsawa-Boris A., Yanagisawa M., Yang I., Yang I.,

Yuan Z., Zavolan M., Zhuu Y., Zammer A., Carninoi P., Hayatsu N.,

Yuan Z., Zavolan M., Sahikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
EMILIN 1 precursor (Elastin microfibril interface-located protein 1)
EMILIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF_01206; -; 1.
InterPro; IPR000512; Oxidored_molyb.
InterPro; IPR006311; Tat.
Pfam; PF00174; oxidored_molyb; 1.
ITGREAGS, TIGR01409; TAT signal_seq; 1.
Hypotherical protein; Complete proteome.
SEQUENCE 339 AA; 37901 MW; B926DFC9AAB49438 CRC64;
                                                                                                                                                                 Nature 417:459-463(2002).
-!- SIMILARITY: Belongs to the UPF0190 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1017 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE011796; AAM36515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.5
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SLLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMI1 MOUSE
Q99K41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MI1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 5
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A Mirraria, T., Wast, K., Kawai, J., Aizawa, K., Artikasa, T., Fibriasa, R. M. Wazaki, A., Yoshino, M., Waterston R., Jahil Y., Tohi, Y., Tohi, Y., Tahili, Y., Tohi, Y., Tahi, Y., Yoshino, M., Waterston R., Jahoffer E.S., Rogers J., Manufala, A., Yoshino, M., Waterston R., Jahoffer E.S., Rogers J., Manufala, A., Yoshino, M., Waterston R., Jahoffer E.S., Rogers J., Manufala, A., Yoshino, M., Waterston R., Jahoffer E.S., Rogers J., Manufala, A., Yoshino, M., Waterston R., Jahoffer E.S., Rogers J., Manufala, M., Yoshino, M., Manufala, M., Manufala, M., Yoshino, M., Manufala, M., Manufal
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succinoglycan biosynthesis.";
J. Bacteriol. 175:7045-7055(1993).
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Interpro; IRR001073; Clq.
Interpro; IRR008983; TW_like.
Pfam; PF01386; Clq; 1.
Pfam; PF01391; Collagen; 1.
Cell adhesion; Extracellular matrix; Signal; Coiled coil; Collagen; Glycoprotein.
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MEDLINE=94042870; PubMed=8226646;
Glucksmann M.A., Reuber T.L., Walker G.C.;
"Genes needed for the modification, polymerization, export, and processing of succinoglycan by Rhizobium meliloti: a model for
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"Family of glycosyl transferases needed for the synthesis of succinoglycan by Rhizobium meliloti.";
". Bacteriol. 175:7033-7044(1993)
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 21, Last annotation update)
8-FEB-2003 (Rel. 41, Last annotation update)
Succinoglycan blosynthesis transport protein exof.
EXOT OR RB1074 OR SMB20950.
Rhizobium mellioti (Sinorhizobium mellioti).
Rhizobium mellioti (Sinorhizobium mellioti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Pred. No. 66;
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MEDLINE=94042869; PubMed=8226645;
                                                                                                EMBL; AK029337; BAC26403.1; -. EMBL; BC005481; AAH05481.1; -. MGD; MGI:1926189; Emilin1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL Outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                          Puehler A.;
"Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT, and exol involved in exopolysaccharide biosynthesis and nodule invasion: exoU and exoW probably encode glucosyltransferases.";
Wol. Plant Microbe Interact. 6:735-744(1993).
                                                                                                                                                                                                                                                                                  Finan T.M., Weidner S., Wong K., Bubrmester J., Chain P., Finan T.M., Weidner S., Wong K., Bubrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Vorhoelter F.J., Hernandez-Lucas I., Backer A., Cowie A., Gouzy J., Golding B., Puehler A.;

"The complete sequence of the I,633-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinoptium meliloci.",

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

-!- PATHWAY: Exopolyyaaccharide biosynthesis a

-!- SABTELLULAR LOCATION: Integral membrane protein (Probable).

-!- SIMILARITY: Belongs to the polysaccharide synthase family.
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SEQUENCE FROM N.A.
STRAIN-BCR2011 / S147;
MEDLINE-94162682; PubMed=8118055;
Becker A., Kleickmann A., Kuester H., Keller M., Arnold W.,
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Pred. No. 52;
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Exopolysaccharide synthesis; Transmembrane; Plasmid;
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ID CUTI BOTCI STANDARD; PRT; 202 AA.
Q00299;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
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PIR; B95976; B95976.
PIR; C49349; C49349.
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M. Kawai U., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., A Mazhinas-Ziuobsebi, PubMeda I. Adachi U., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi U., Fukuda S., Alaxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Ashburner M., Batalov S., Kochiwa H., Sakuli P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackehbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F., Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Whittaker C., Wilming L., Whanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                  Inoue S., Sano H., Ohta M., "Growth suppression of Expression of "Growth suppression of Escherichia coli by induction of expression of mammalian genes with transmembrane or ATPase domains."; Blochem. Blophys. Res. Commun. 268:553-561(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Small intestine;
MEDLINE=21085660; PubMed=11217851;
                                                  MEDLINE=20145471; PubMed=10679242;
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                             CUTA.

Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).

Butrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).

Butryotis, Fungi, Ascomycota, Pezizomycotina, Leotiomycetes, Helotiales, Sclerotiniaceae, Botryotinia.

NCBI_TaxID=40559;
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10-OCT-2003 (Rel. 42, Last annotation update) Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
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Pfam; PF01083; Cutinase; 1.
PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE 1; 1.
PROSITE; PS00931; CUTINASE 2; 1.
Hydrolase; Serine esterase; Signal, SIGNAL
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HSSP; P00590; 1XZJ.
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Best Local Similarity 66.7
Matches 6; Conservative
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TISSUES ETROM N.A.

TISSUES Salivary gland;

MEDINNELS288257; PubMed=12477932;

MEDINNELS288257; PubMed=12477932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.L., Manuella F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A thicknil S.F., Zeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B tacheroko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

Rask S.A., McEwan P.J., McKerran S., Garcia A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A villaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield M. S. Wong M. Schmutz J. Marra M.A.,

Butterfield W.S.N., Krzywinski W.I., Marra M.A.,

Butterfield W.S.N., Krzywinski W.I., Marra M.A.,

Butterfield W.S.N., Krzywinski W.I., Marra M.A.,

Butterfield W.B., Wolley M. Schmutz J. Marra M.A.,

Butterfield W.B., Wolley M. Wolley M. Schmutz J. Warra M.A.,

Butterfield W.B., Wolley M. Wolley M. Schmutz J. Warra M.A.,

Butterfield W.B., Wolley M. Wolley M. Warra M.A.,

Butterfield W.B., Wolley M. Wolley M. W. Warra M.A.,

Butterfield W.B., Wolley M. W.,

Butterfield W.B., Wo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB030183; BAA92747.1; -.
EMBL; AK008109; BAB25465.1; -.
EMBL; BC019547; AAH19547.1; -.
MGD; MGI:1923764; 2010004020Rik.
INCEPPC; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin.
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Gaps

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Mus musculus (Mouse). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI\_TaxID=10090;

10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)

STANDARD;

CG21 MOUSE

G21\_MOUSE

O9JMG3;

Protein C7orf21 homolog.

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GPDA_TRYBB
P90593;
                                                                                                                                                                                      DOMAIN
                                                                                                           TRANSMEM
TRANSMEM
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                                                                                                                                                 TRANSMEM
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
GPDA_TRYBB
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney, and Placenta;

TISSUE-Kidney, and Placenta;

TISSUE-Kidney, and Placenta;

MEDINE-238825; PubMed=1247932;

MEDINE-238825; PubMed=1247932;

MISCANI S. PubMed=1247932;

MISCANI S. PubMed=1247932;

MISCANI S. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S. Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasheh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Mapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Uddin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.M., Glabs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Glabs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Glabs R.A.,

Millalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butkeriled Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Meneration and initial analysis of more than 15,000 full-length human and mouse only a sequences.",

From Marl A. Schein J.B., 18, A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                            .
0
                                                                                                                                                                                      Score 31; DB 1; Length 245;
Pred. No. 42;
1; Mismatches 1; Indels
                                                                      POTENTIAL.
POTENTIAL.
UBIQUITIN-LIKE.
LEU-RICH.
*/ 02C1D1B24C13139D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang W., Li N., Wan T., Zhang M., Cao X.,
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein C7orf21 (SB144).
                                                                                                                                                                                                                                                                                                                                                                                                   246 AA.
                                                        POTENTIAL
                  PROSITE; PS50053; UBIQUITIN_2; 1.
Transmembrane.
                                                    11 31 POT
194 214 POT
219 239 POT
102 175 UBI
197 238 LEU
245 AA; 26316 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY037155; AAK67645.1; -. EMBL; BC000936; AAH00936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                      Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
UBO; 1.
                                                                                                                                                                                                                                                                                                     196 SLLIPLLL 204
                                                                                                                                                                                                                                                                 1 STITTS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
  SMART; SM00213;
                                                                                                                                                                                                                                                                                                                                                                                                     CG21 HUMAN
                                                      TRANSMEM
TRANSMEM
TRANSMEM
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            ESULT 9
G21_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=427;
MEDLINE=97071437; PubMed=8920004;
Kohl L., Drmota T., Thi C.D., Callens M., van Beeumen J.,
Copperdoes F.R., Michels P.A.M.;
"Cloning and characterization of the NAD-linked glycerol-3-phosphate
dehydrogenases of Trypanosoma brucei brucei and Leishmania mexicana
mexicana and expression of the trypanosome enzyme in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(+) = glycerone phosphate + NADH.
-1- SUBCELLUIAR LOCATION: Glycosomal.
-1- SIMILARITY: Belongs to the NAD-dependent glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
Glycerol-3-phosphate dehydrogenase [NAD+], glycosomal (EC 1.1.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 1; Length 246;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                UBIQUITIN-LIKE.
LEU-RICH.
E08E25A6B37665B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37783 MW; 12CE19AEDA9E4EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 AA
                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biochem. Parasitol. 76:159-173(1996).
                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR008927; 6DGDH C like.
InterPro; IPR006468; NAD G137B dh.
InterPro; IPR006409; NAD G137B dm.
Pfam; PP01210; NAD G137B dh; 1.
PRINTS; PR00077; GPDHDRONASE.
PRODOM; PD001278; NAD G137B dom; 1.
PROSITE; PS00957; NAD G137B dom; 1.
EMBL, BC033182, AAH33182.1; -. Genew, HGNC:21709, Crorf21.
ThterPro. PRO0626; Ubiquitin.
Pfam, PF00240; ubiquitin, 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Glycosome
                                                                                                                                                                                                                                                                                                            26261 MW;
                                                                                                                                                                                                                                                                                                                                                       77.5%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                      31
215
241
176
239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 SLLLPLLL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLLLPLQIL 9
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                                                                                                                                                                                               195
221
221
103
198
246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                  PROSITE; PS50
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Length 354;

DB 1;

77.5%; Score 31;

Pred. No. 60;

77.8%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ViTat 1.1;
MEDLINE=97077436; PubMed=8920003;
Stebeck C.E., Frevert U., Mommsen T.P., Vassella E., Roditi I.,
Pearson T.W.;
"Moleoular characterization of glycosomal NAD(+)-dependent glycerol 3-
phosphate dehydrogenase from Trypanosoma brucei rhodesiense.";
Mol. Biochem. Parasitol. 76:145-158(1996).
-!- CATALYIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(+) = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma brucei rhodesiense.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=31286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                   Gabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 354 MICROBODY TARGETING SIGNAL (POTENTIAL).
354 AA; 37834 MW; OCEO49C5E8F83C00 CRC64;
                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glycerol-3-phosphate dehydrogenase [NAD+], glycosomal (EC 1.1.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBSELLUTAR LOCATION: Glycosomal.
-!- SIMILARITY: Belongs to the NAD-dependent glycerol-3-phosphate dehydrogenase family.
                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 12
FUD ECCLI STANDARD; PRT; 428 AA.
D _YFUD_ECCLI STANDARD; P7009;
T 01-OCT-1994 (Rel. 30, Created)
T 15-DEC-1998 (Rel. 37, Last sequence update)
T 16-DCCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yfjD.
N YFUD OR B2612/B2613.
                                                                                                                                                                                                                                                                          354 AA.
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X91142; CRA62581.1; -.
InterPro; IPR008927; 6DGDH C like.
InterPro; IPR006168; NAD GIy3P dh.
InterPro; IPR006109; NAD GIy3P dh.
Pfam; PF01210; NAD GIy3P—dh; L.
PRINTS; PR00077; GPDHDRGNASE.
PROGOM; PD001278; NAD GIy3P—dm; 1.
PROSITE; P800957; NAD GI93P, 1.
Oxidoreductase; NAD; GIy3P—dom; 1.
                                                                                                                                                                                                                                                                          PRT;
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                   124 ŚLLFPAĢIL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLLFPAQIL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphate + NADH.
                                                                               1 STITTETOIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e riordrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; NAD;
SITE 352 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          TRYBR
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                                                                                                                                                                                                                                                                                                    STRAIN=K12;
MEDLINE=9734980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Mixi T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Mixi T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Satto N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia coli-
KI2 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipinska B., King J., Ang D., Georgopoulos C., "Sequence analysis and transcriptional regulation of the Escherichia coli grpE gene, encoding a heat shock protein."; Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS 2 CBS domains.
-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 199 THAT PRODUCES TWO ORFS.
-1- CAUTION: Ref.3 sequence differs from that shown due to numerous frameshifts.
                                                                                                    STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                    Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO
H.INFLUENZAE H10107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000347; AAC75661.1; ALT FRAME.
EMBL; AE000347; AAC75661.1; ALT FRAME.
EMBL; D90888; BAA16497.1; ALT INIT.
EMBL; X07863; -; NOT ANNOTATED_CDS.
ECGENE; EG12442; yfjD.
INTERPO; IPR003550; CBS.
INTERPO; IPR000544; CBS domain.
INTERPO; IPR005170; COrC_transpt-asc.
Fram; PF03471; COrC_HIYC; 1.
SYART; SM00116; CBS; 1.
Hypothetical protein; CBS domain; Repeat.
TRANSMEM 65 88 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rudd K.E.;
Unpublished observations (AUG-1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88319942; PubMed=3045760;
                  Bacteria, Proteobacteria, Gammar
Enterobacteríaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 322-428 FROM N.A.
                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION.
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112 BOV:
                                                                                                                                                                                                                                                                                                              RESULT 14
IL2_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=9235200; PubMed=1321427;

Ravid S., Spudich J.A.;

Transe-bound Dictyostelium myosin heavy chain kinase: a developmentally regulated substrate-specific member of the protein kinase C family.";

L. Proc. Natl. Acad. Sci. U.S.A. 89:5877-5881(1922).

L. Proc. Natl. Acad. Sci. U.S.A. 89:5877-5881(1922).

L. PRINCTION: Brings about phosphorylation of specific threonines in the heavy chains of myosin during chemotaxis, which results in inhibition of myosin thick filament formation. Phosphorylation also inhibite the actin-activated ATPase activity of myosin.

C. -I- CATALYTIC ACTIVITY: ATP + [myosin heavy-chain] = ADP + [myosin heavy-chain] phosphate.

C. -I- SUBCELIULAR LOCATION: Membrane-bound.

C. -I- BEVELOPMENTAL STAGE: Expressed only during development.

C. -I- SIMILARITY: Belongs to the eukaryotic diacylglycerol kinase
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
-!- CAUTION: While this is experimentally defined to be a protein kinase, it could be, on the basis of sequence similarities, a diacylglycerol kinase.
                                                                                     ö
                                                     77.5%; Score 31; DB 1; Length 428; 87.5%; Pred. No. 72; cive 0; Mismatches 1; Indels
                POTENTIAL.
38456865EDBCB151 CRC64;
                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosli heavy chain kinase (EC 2.7.1.129) (MHCK).
                                                                                                                                                                                                                   783 AA
   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DictyBase; DDB0185000; M93393.
InterPro; IPR00219; DAG PE-bind.
InterPro; IPR001219; DAG PE-bind.
InterPro; IPR001206; DAGKc.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00699; DAGKa; 1.
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M93393; -; NOT ANNOTATED CDS
 92 112 PC
130 150 PC
428 AA; 48044 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002939; DAGKa; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00109; C1; 2.
SMART; SM00045; DAGKa; 1.
SMART; SM00046; DAGKC; 1.
                                                                                       Conservative
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                                                        Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                  _KWHC_DICDI
P34125;
01-FEB-1994
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family
                TRANSMEM
   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
PROSITE; PS00479; DAG PE BIND DOM 1; 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 2.

Transferame; Serine/fhreozine-profein; Repeat.

DOMAIN 19 69 PHORBOL-ESTER AND DAG BINDING 1.

PHORBOL-ESTER AND DAG BINDING 2.

PHORBOL-ESTER AND DAG BINDING 2.

NP BIND 466 474 ATP PRORBOL-ESTER AND DAG BINDING 2.

DOMAIN 489 489 ATP (BY SIMILARITY).

DOMAIN 186 196 ASN-RICH.

DOMAIN 754 773 SER/THR-RICH.

PHOSPHORYLARION (AUTO-) (BY SIMILARITY).

SEQÜENCE 783 AA; 89154 MM; 6CAFI77F4436F43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D., Gillis S., Cosman D., Baker P.E., "Cloning, sequence, and expression of bovine interleukin 2."; Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL2 OR IL-2.
Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=86205870; PubMed=3486415;
Reeves R., Spies A.G., Nissen N.S., Buck C.D., Weinberg A.D.,
Barr P.J., Magnuson N.S., Magnuson J.A.;
"Molecular cloning of a functional bovine interleukin 2 cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 783;
Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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EMBL; M13204; AAA21143.1; ALT_INIT
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 SLLNPLQII 244
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Bur. J. Immunogenet. 29:341-345(2002).

FuncTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can simulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEQUENCE FROM N.A. MEDINE-2117121282; MEDINE-22117321; PubMed=12121282; Sreekumar E., Premraj A., Saravanakumar M., Rasool T.J.; Sreekumar E., Premraj A., Saravanakumar E., sequence analysis reveals "Buffalo (Bubalus bubalis) interleukin-2: sequence analysis reveals high nucleotide and amino acid identity with interleukin-2 of cattle
                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-2.
BY SIMILARITY.
O-LINKED (GALLAC. . .) (BY SIMILARITY).
O-A (IN REF. 2).
1 816667DFEA052EDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bubalus bubalis (Domestic water buffalo).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bommalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bubalus.
ENEL; X52687; CAA36912.1; -..
PIR; 145913; 145913.
HSSP; 901585; 31NK.
InterPro; IRF00079; Interleukin-2.
PRINTS; PR00255; INTERLEUKIN2.
PRODID: PROOF 99; Interleukin-2; 1.
SYART; SM00189; II.; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
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OCT--2003 (Rel. 42, Last sequence update)
O-OCT--2003 (Rel. 42, Last annotation update)
interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1; Length 155;
Pred. No. 43;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF363786; AAK50039.1; -.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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21 155 IN
79 127 BY
23 0-1
66 66 V V
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                  BY SIMILARITY.
INTERLEUKIN-2.
BY SIMILARITY.
O-LINKED (GALNAC. . .) (BY SIMILARITY)
1753173FE619946B CRC64;
PROSITE; PS00424; INTERLEUKIN_2; 1.
Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                                      ô
                                                                                                           75.0%; Score 30; DB 1; Length 155; 77.8%; Pred. No. 43; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                           Search completed: March 1, 2004, 17:29:59
Job time : 7 secs
                                1 20 BY
21 155 INT
79 127 BY
23 23 0-1
155 AA; 17541 MW;
                                                                                                                                        Conservative
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Best Local Similarity
Matches 7; Conserv
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CARBOHYD
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SIGNAL
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emericella

Q92255 mus musculu Q92255 mus musculu Q96883 mus musculu Q35426 mus musculu Q35426 mus musculu Q35426 mus musculu Q36416 porphyromon Q86166 porphyromon Q8616 parcharomyc Q9690 giardia lam Q98x56 arabidopsis Q81149 arabidopsis Q81149 arabidopsis Q81149 arabidopsis Q81149 arabidopsis Q81149 musculum Q98x16 xanthomonas Q98x66 xanthomonas Q98x66 xanthomonas

Q9vyn0 drosophila Qx620 salmonella O76155 periplaneta Q84bf5 xanthomonas Q8wx77 homo sapien O22910 arabidopsis

Q8u6y8 agrobacteri Q82vh0 nitrosomona Q9kal1 bacillus ha P96675 bacillus su

Q9v3y4 drosophila Q9mms8 syrigma sib

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Gaps

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 4; Length 253; 100.0%; Pred. No. 3.7; ive 0; Mismatches 0; Indels
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GO: GO: 0004255; F: chymotrypain activity; IEA.
GO: GO: 0004255; F: trypain activity; IEA.
GO: GO: 0004255; F: trypain activity; IEA.
GO: GO: 0006259; F: trypain activity; IEA.
GO: GO: 0006508; P: proteclysis and peptidolysis; IEA.
InterPro: IPR009003; Cys Ser_trypsin.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001254; Peptidase_S1.
RPINTS; PR001254; Peptidase_S1A.
RPINTS; PR00125; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.
RPOSITE; PS00135; TRYPSIN_DOM; 1.
RPOSITE; PS00135; TRYPSIN_DOM; 1.
RPOSITE; PS00135; TRYPSIN_DOM; 1.
RPOSITE; PS00135; TRYPSIN_ER: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC032005; AMH32005.1; antivity: IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 7 (chymotryptic, stratum corneum)
Homo sapiens (Human)
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Q8PKF6
Q8ZUD7
                                         035426
035426
09R1S4
09M0J5
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Q12212
Q969D0
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Q8LWX9
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09KAL1
P96675
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Q84BF5
Q8WX77
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971148
971149
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Skin;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
QBN5N9
   SO ON THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8vca9 mus musculu Q8r5d6 mus musculu Q8r5d6 mus musculu Q8r5d6 prucella me Q8fzx1 brucella su Q7u3j6 synechococo Q7v4d prochloroco Q819m8 bacillus ce Q8vbb6 white spot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7u5r4 synechococc
Q9d226 mus musculu
Q9zte3 arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7wxy8 pseudomonas
Q8brv0 mus muscul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9v2d5 pyrococcus
O21527 clethrionom
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                                                                                                        Description
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              otal number of hits satisfying chosen parameters:
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Q9V2D5
Q9V2D5
Q8VCA9
Q8R5D6
Q8YHY9
Q8FZX1
Q7V94G
Q7V94G
Q19M8
Q8VBB6
Q7WXY8
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Q7U5R4
Q9D226
Q9ZTE3
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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Q8R5D6
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Mol. Biol. EVOI. 15:35-49(1998).

Mol. Biol. EVOI. 15:35-49(1998).

EMBL: UR3808; AABBT168.1;

GO; GO:00085739; C:mitochondrion; IEA.

GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0016491; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0016491; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0016120; P:mitochondrial electron transport, NADH to u. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Pyrococus abyssi genome sequence: insights into archaeal chromosome structure and evolution "; Submitted (ULL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ748283; CAPA9063.1; -. PIR; H75201; H75201.
                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clethrionomys gapperi (Southern red-backed vole).
Mitochodrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Arvicolinee;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0xADH dehydrogenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone)
0x1doreductase chain 4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIR; H/54U1; H/54U1.
InterPro; IPR008537; DUF819.
Pfam, FF05684; DUF819; 1.
Pypothetical protein; Complete proteome.
SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;
                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein PYRAB01390.
PYRAB01390 OR PAB01088.
Pyrococcus abyssi.
                                                                                                                                        146 AA
                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
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InterPro; IPR001750; Oxidored q1.
InterPro; IPR000260; Oxidored q5_N.
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Matches 8; Conservative
                                                                                                                                      PRELIMINARY;
                          4 SLLLPLOIL 12
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1 SILLPLOIL 9
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STRAIN=GE5 / Orsay;
Heilig R.;
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NCBI_TaxID=56223;
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NCBI_TaxID=29292;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
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Pred. No. 20;
1; Mismatches 0; Indels
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92.5%; Score 37; DB 8; Length 208;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Salivary gland;
Strausberg R.;
Submitted (GAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -.
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
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InterPro; IPR001179; FKBP_PPIase.
Pfan; PF00254; FKBP; I.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF01059; oxidored_q5 N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
NON TER 208 208
SEQÜENCE 208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN cDNA 1110002023 gene.
FKBP11 OR 1110002023RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
similar to RIKEN CDNA 1110002033 gene.
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87.5%; Pred. No. 27;
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Best Local Similarity 87.55,
Best Local 7; Conservative
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379 AA
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Best Local Similarity 75...
6; Conservative
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PIR; AB3334; AB3334.
TIGR; BR1349; -.
Complete proteome.
SEQUENCE 370 AA; 4
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Q7V4U4;
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Q7U9J6;
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MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
Read T.D., Dodson R.J., Umyam L., Erinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Riedmuller, S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
"The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S. A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                STRAIN-16M / ATCC 23456 / Biotype 1;

MEDLINES-20020109; PubMed=11756688;

DelVecchio V.G., Kapelar R.J., Patra G., Mujer C., Los T.,

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
   Gaps
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Pred. No. 1.4e+02;
2; Mismatches 0; Indels
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Brucellaceae, Brucella.
NCBI_TaxID=29461,
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Brucellaceae, Brucella.
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                                                                                                                                          01-MAR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Daunorubicin resistance transmembrane protein.
BMEI0556.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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BR1349.
   1; Mismatches
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   7; Conservative
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                             LLLPLQIL 9
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Best Local Similarity
Matches 6; Conserv
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Palenik B., Brahameha B., Lariner F.W., Land M., Hauser L., Chain P.,
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Dufresne A., Partensky F., Webb E.A., Waterbury J.;
The genome of a montile marine Synechococcus.";
Mature 424:1037-1042(200)
EMBL; BX569689; CAE06775.1;
Glycosyltransferase; Signal; Transferase; Complete proteome.
SIGNAL
SIGNAL
19 Potential.
SEQUENCE 379 AA, 40174 MW; 98D697ECEF71C73F CRC64;
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Anlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
"Genome divergence I.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424:1042-1047(2003).
NATURE 424:1042-1047(2013).
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
                                                        Length 370;
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                                1; Indels
40369 MW; 819AAD684305CB60 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Glycosyl transferase, family 4 precursor (BC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycosyltransferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.5%; Score 33; DB 16;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1;
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"Identification of a nucleocapsid protein (VP35) gene of shrimp white spot tyndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
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MEDILINE=2017548; PubMed=11062040;
MEDILINE=2017548; PubMed=11062040;
Taai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot syndrome virus (WSOV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21844011; PubMed=11853398;
Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
MEDLINE=21548311; PubMed=11689662;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          He J., Rahme L.G.;
"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY273869; AAP84197.1; -.
SEQUENCE 78 AA, 8977 MW; 9B37EF21434C91A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 12; Length 72;
Pred. No. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Taiwan;

Lo C.-F., Kou G.-H.;

Submit-Led (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF332093; AAL33056.1; -.

EMBL; AF440570; AAL88977.1; -.
                                                                                                                         SEQUENCE FROM N.A.
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7862 MW; E84A9814F2D7581A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pre
                                                                                   Virol. 75:11811-11820(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LLLPLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PA14;
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Matches
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GO; GO:0016020; C:membrane; IEA.
GO; GO:000511; F:sodium:dioarboxylate/tricarboxylate symport. . .; IEA.
GO; GO:000511; F:sodium:dioarboxylate/tricarboxylate symport. . .; IEA.
GO; GO:0000910; F:sotokinesis; IEA.
GO; GO:0006835; P:dicarboxylic acid transport; IEA.
InterPro; IPR001182; Cell cycle.
InterPro; IPR001991; Na/dICO_symport.
InterPro; IPR006162; Ppantne.
FP01098; FTSW_RODA_SPOVE; 1.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22608415; PubMed=12721630; Ivanova N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A., Grechkin Y., Busch G., Haselkorn R., Fonstein M., Bhrlich S.D., Overbeek R., Kyrpides N.; Coreckin Y., Strinch S.D., Genome sequence of Bacilus cereus and comparative analysis with Mature 423:87-91(2003).
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    Glycosyltransferase; Signal; Transferase; Complete proteome.
SIGNAL 1 19 Potential.
SEQUENCE 381 AA; 40217 MW; 4DBAB55F313F8BEZ CRC64;
                                                                                        Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 392;
                                                                                   Score 33; DB 16; Length 38
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                           0819M8 PRELIMINARY, PRT, 392 AA.
0819M8.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Eatl division protein ftsW.
BRO348.
BRO311us cereus (strain ATCC 14579 / DSM 31).
BRO451 Firmicutes, Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0173; EDTRNSPORT.
PROSITE; PS00428; FTSW RODA SPOVE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
CELL division; Complete proteome.
SEQUENCE 392 AA; 42797 MW; 7AAA58737762F659 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Msy052 (WSSV109).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.5%; Score 33; DB 16;
88.9%; Pred. No. 1.5e+02;
cive 0; Mismatches 1;
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                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                       1 SLLLPLOIL 9
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SEQUENCE FROM N.A.
                          SIGNAL
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ESULT 11 28VBB6

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Chaperone; Repeat
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RESULT 15
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                                                                                   01-MAR.2003 (TrENBLrel. 23, Created)
01-MAR.2003 (TrENBLrel. 23, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
Hypothetical protein.
Wus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
NUCEL_TAXID=10090;
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80.0%; Score 32; DB 11; Length 102;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels
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80.0%; Score 32; DB 16; Length 17

Best Local Similarity 77.8%; Pred. No. 1.1e+02;

Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                            al protein.
102 AA; 12058 MW; 9FCD4A6CA10276A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                         $\tilde{0.105R4};$$\tilde{0.105R4};$$\tilde{0.105R4};$$\tilde{0.105R-2003}$$(TEMBLrel. 25, Created)$$$01-0CT-2003 (TEMBLrel. 25, Last sequence update)$$$1-0CT-2003 (TEMBLrel. 25, Last annotation update)$$$$IMPOCHELical protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                     171 AA
                                                                     PRT;
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                    24 SLELPLOVL 32
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 1 SLLLPLOIL
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Gissi C., King B., Kochiwa H., Rochim P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Batak J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Abrincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima U., Mazaraelli J., Mondaerte P., Lyons P., Marchioni L., Mashima M., Rochiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Whittaka Y., Kansuki Y., Wang K., Wang K.H., Weltz C., Whittaker C., Wilming L., Warner, Ano., Re., And., And., Ano., Re., And., 
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                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:0005489; F:chectron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; PR001450; 4Fe45_ferredoxin.
PROSTE; PG0198; 4Fe45_FERREDOXIN; 4.
                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
A030007E19R1k protein.
MUS MUSCALLERER.
     196 AA
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     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=21085660; PubMed=11217851;
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EMBL; AK020699; BAB32180.1; -.
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Best Local Similarity 66...
6; Conservative
PRELIMINARY;
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145 ALLLPVQLL 153
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Job time : 32.3333 secs
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Sequence 80, App. Sequence 80, App.
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                                                                                                                                   Sequence 4, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 3, Sequence 15,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33
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Sequence 1
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/cgn2 6/prodara/2/iaa/5A_COMB.pep:*
/cgn2 6/prodara/2/iaa/5B_COMB.pep:*
/cgn2 6/prodara/2/iaa/6A_COMB.pep:*
/cgn2 6/prodara/2/iaa/6B_COMB.pep:*
/cgn2 6/prodara/2/iaa/POTUS COMB.pep:*
/cgn2 6/prodara/2/iaa/POTUS COMB.pep:*
/cgn2 6/prodara/2/iaa/POTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-146-831-19
PCT-US96-09303-19
US-08-096-946-10
US-08-096-946-11
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US-08-557-146-12
US-09-154-344-12
US-09-644-600-4
US-09-654-600A-4
US-08-824-60A-4
US-08-824-84-3
US-08-824-844-3
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US-08-768-859A-16
US-08-768-859A-21
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US-09-210-084-3
US-09-764-762-3
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US-09-679-279-15
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Maximum Match 100%
Listing first 45 summaries
                                                                                             M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
                                                                                                                                                                                                                           US-09-905-083-80
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erfect score:
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80.0 237 3 US-08-767-820A-16 Sequence 1, Appli 80.0 237 3 US-08-767-820A-16 Sequence 16, Appli 80.0 237 3 US-08-622-0A6B-1 Sequence 16, Appli 80.0 237 3 US-08-622-0A6B-1 Sequence 1, Appli 80.0 237 3 US-08-622-0A6B-7 Sequence 1, Appli 80.0 237 3 US-08-622-0A6B-7 Sequence 7, Appli 80.0 237 3 US-08-944-483-38 Sequence 37, Appli 80.0 237 3 US-09-100-264-1 Sequence 37, Appli 80.0 237 3 US-09-100-264-1 Sequence 37, Appli 80.0 237 3 US-09-100-264-1 Sequence 37, Appli 80.0 237 4 US-09-100-264-1 Sequence 1, Appli 80.0 237 4 US-09-303-39-1 Sequence 1, Appli 80.0 237 4 US-08-843-076b-7 Sequence 7, Appli 80.0 237 4 US-08-843-076b-7 Sequence 7, Appli 80.0 237 4 US-08-843-076b-7 Sequence 7, Appli 80.0 237 5 US-09-303-208-1 Sequence 1, Appli 80.0 237 5 US-09-303-208-1 Sequence 1, Appli 80.0 237 5 PCT-US94-07329-10 Sequence 11, Appli 80.0 237 5 PCT-US94-07329-10 Sequence 11, Appli 80.0 237 5 PCT-US94-07329-11	ALIGNMENTS	RESULT 1 US-09-502-600-80 Sequence 80. Application US/09502600A Sequence 80. Application US/09502600A GENERAL INFORMATION: APPLICANT O' Brien, Timothy J. TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis on TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D62231P-C CURRENT PILING DATE: 2000-02-11 CURRENT APPLICATION NUMBER: US/09/502,600A FRICR APPLICATION NUMBER: US/09/502,600A PRICR FILING DATE: 03-14-1998 NUMBER OF SEQ ID NOS: 136 SEQ ID NO 80 LENGTH: 9 TYPE: PRT CORGANISM: Homo sapiens FRATURE: FRATURE: CHER INFORMATION: Residues 207-215 of the SCCE protein US-09-502-600-80	n 100.0%; Score 50; DB 3; Length 9; Similarity 100.0%; Pred. No. 3e+05; 9; Conservative 0; Mismatches 0; Indels 0; Gaps	GPLVCRGIL 9          GPLVCRGIL 9	RESULT 2 US-09-918-243-80  Sequence 80, Application US/09918243  Patent No. 6627403  GENERAL INFORMATION:  APPLICANT: O'Brien, Timothy J.  APPLICANT: Santin, Martin J.  APPLICANT: Santin, Alessandro  TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer  TITLE OF INVENTION: WOMBER: US/09/918,243  CURRENT FAPLICATION NUMBER: US/09/918,243  CURRENT FILING DATE: 2001-07-30  PRIOR PLING DATE: 2001-07-30  PRIOR PLING DATE: 2001-07-13  NUMBER OF SEQ ID NOS: 136  SEQ ID NO 80  LENGTH: 9  LENGTH: 9  TYPE: PRT  CREANISM: Homo sapiens
00000000000000000		-600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80 -600-80	atc]	1 GPLVCI          GPLVCI	-243-80 e 80, Appl. No. 662740 No. 662740 ANT: Cann. CANT: CANT. C
8 4 6 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		RESULT 1 US-09-502 Sequence GENERAL APPLICA TITLE TITLE FILE R CURREN PRIOR PR	Query Ma Best Loc Matches	. දු	RESULT 2 US-09-918-243- Sequence 80. Sequence 80. Septent No. 6 GENERAL INC. APPLICANT: PRICE REFERSE CURRENT APPLICANT: PRICE REFERSE CURRENT PIL PRICE APPLICANT: PRICE APPLICANT: PRICE APPLICANT: APPLICANT: TYPE: PRICE APPLICANT:

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178 GPLVCRGTL 186

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US-08-557-146-12; Sequence 12, Application US/08557146; Patent No. 5834290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                              Sequence 33, Application US/08944483
Sequence 33, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COLETY, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: ADDOLT Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                   100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein
S-09-918-243-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                         1 GPLVCRGTL 9
                                                                                                                                                                              GPLVCRGTL 9
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1 GPLVCRGTL 9

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0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: SCCE
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                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPLVCRGTL 9
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Best Local Similarity
Matches 9; Conserv
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Recombinant Stratum Corneum Chymotryptic
Enzyme (SCCE)
                                                             Score 50; DB 2; Length 225;
Pred. No. 0.14;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 2; Length 225; 100.0%; Pred. No. 0.14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ER PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
CLASSIFICATION:
PRIOR DATE: 14-DEC-1995
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corn
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
; OTHER INFORMATION: similar domain in TADG-15 JS-09-027-337-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1103326-181
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Patent No. 5981256
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IS-09-644-600-4
Sequence 4, Application US/09644600
Settent No. 6451500
GENERAL INFORMATION:
APPLICANT: 0'Erien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFRENCE/DOCKET NUMBER: 11033
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEGUINCE CHARACTERISTICS:
LENGTH: 225 amino acids
                                                                                                    ;
0
                                                             Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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MOLECULE TYPE: polypeptide
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Best Local Similarity 100.
Matches 9; Conservative
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Gaps
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Sequence 4, Application US/09654600A

Sequence 4, Application US/09654600A

Patent No. 6649741

GENERAL INPORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: TARG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TOVEREXPESSED IN CARCINOMAS

TITLE OF INVENTION: TOVEREXPESSED IN CARCINOMAS

TITLE OF INVENTION: TOVEREXPESSED IN CARCINOMAS

CURRENT APPLICATION WINBER: US/09/654,600A

CURRENT PILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: Overexpressed in Carcinomas FILE REFERENCE: D6064C1PD/D CURRENT APPLICATION NUMBER: US/09/644,600 CURRENT FILING DATE: 2000-08-23 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR FILING DATE: 1999-10-20 PRIOR FILING DATE: 1999-10-20 PRIOR FILING DATE: 1999-02-20 NUMBER OF SEQ ID NOS: 98 LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 4; Length 225; Conservative 0; Minner.
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Sequence 2, Application US/09154344 Patent No. 5981256
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
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      TELEFAX: 415-845-4166
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GPLVCRGTL 215
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LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                                                                                                                      US-08-824-874-3
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ADDA...
STREET: A...
CITY: New York
CUMTR: New York
COUNTR: U.S.A.
ZIP: 10.56-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/ASDNT INFORMATION:
NAME: Sterner: Richard J.
REGISTRATION NUMBER: 35,372
RESTERNEG-DOCKET NUMBER: 35,372
REGISTRATION INFORMATION:
TELEPAM: (212) 819-8783
TELEPAM: (212) 819-8783
TELEPAM: (212) 84-8113
INFORMATION FOR SEQ ID NO: 2:
"TH: 23 amino acids
"TH: 23 amino acids
"TH: 25 amino acids
"TH: 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: BR ESTERNI DOS
SOFTWARE: FASTERNI DOS
SOFTWARE: FASTERNI DOS
SOFTWARE: FASTERNI DOS
SOFTWARE: FASTERNI DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: FILEd Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENERAL INPORMATION:

CENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3144 Porter Drive
CITY: Palo Alto
COUTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Patent No. 5962300
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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| Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents | Industrial contents
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207 GPLVCRGTL 215
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COUNTRY: USA
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                                                        Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT:
JOHNSTON:
APPLICANT:
LITLE OF INVENTION:
AMTIOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: AMTIOID PRECURSOR
NUMBER OF SEQUENCES:
ADDRESSES:
ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 50; DB 3; Length 253; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-210-084-3
Sequence 3, Application US/09210084
Sequence 3, Application US/09210084
Setent No. 61272101
PAPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRICR APPLICATION DATA:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: 38,082
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANS: 317-277-1090
TELEFRANS: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: Amino acids
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Best Local Similarity 100.0
Matches 9; Conservative
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COUNTRY: US
ZIP: 94304
ESULT 12
S-08-930-188-2
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MCONFUTER NEADBLE FORE:

MCDITUR TYPE: Liskette

COMPUTER THE COMPANIES.

MCDITURE THE COMPANIES
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CT-US96-04294-2
Sequence 2. Application PC/TUS9604294
GENERAL INFORMATION:
    APPLICANT: Johnstone, Eric P.
    APPLICANT: Johnstone, Edward M.
    APPLICANT: Johnstone, Sheila P.
    TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
    TITLE OF INVENTION: RELATED NUCLEIC ACIDS
    NUMBER OF SEQUENCES:
    ADDRESSER: Bli Lilly and Company
    STREET: Lilly Corporate Center
    CITY: Indianapolis
    STREET: Lilly Corporate Center
    CITY: Indianapolis
    STREET: Lilly Corporate Center
    CITY: United States of America
    ZIP: 46285
COMPUTER: READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: EDM PC Compatible
    OPPRAARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US 08/416,257
    FILING DATE: 04-APR-1995
    ATTORNEY/AGENT INFORMATION:
    RESERENCE/DOCKET NUMBER: 38,082
    RESERENCE/DOCKET NUMBER: 38,082
    RESERENCE/DOCKET NUMBER: 38,082
    RELEPHONE: 317-277-1090
    TELECOMMUNICATION NUMBER: 317-277-1090
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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: anilo acids
TYPE: acids

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MOLECULE TYPE: protein
CT-US96-04294-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 GPLVCRGTL 215
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Ouery Match 100.0%; Score 50; DB 5; Length 253; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels

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207 GPLVCRGTL 215
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Search completed: March 1, 2004, 17:38:25 Job time : 11.8889 secs

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Ada05738 Human Nov
Ada05736 Human Nov
Ada05744 Human Str
Ada05732 Human Nov
Ada05732 Human Nov
Ada05732 Human Nov
Ada05733 Human Nov
Abb84421 Human Str
Abb84421 Human Str
Abb84420 Human Str
Abb8441 Human Str
Abb84400 Human Str
Abb84400 Protein d
Abr58471 Protein d
Abb17440 Protein d
Abb84420 Porcins S
Ada051326 Human Str
Adb86484 Ovarian c
Adb84420 Porcins S
Ada0513752 Novel hum
Aau123217 Novel hum
Aau17043 Human HSC
Abb86011 Connectiv
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                                                                             March 1, 2004, 17:16:55 ; Search time 45.5556 Seconds (without alignments) 55.820 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aae08285 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                      1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                     otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          1586107 segs, 282547505 residues
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                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2
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                                                                                                                                          US-09-905-083-80
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Match Length DB
                                                                                                                                                                    1 GPLVCRGTL 9
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                                                                                                                                                      erfect score:
                                                      M protein
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1969 Human	Abr55400 Amino aci	Aaul6971 Human nov	Aab21297 Human KLK	Aab21305 Human KLK	Abb84419 Bovine SC	Aab21306 Human KLK		Abg19361 Novel hum	Human	_	Abp66315 Bifidobac	Aab82214 Polyketid		Aay48056 Immunogen	Aaw58064 Human pro	m	Aaw11019 Antigen p		Ada50560 Prostate
<b>C</b>	ABR55400	AAU16971	AAB21297	AAB21305	ABB84419	AAB21306	ABJ26666	ABG19361	ABB84409	AAB11713	ABP66315	AAB82214	AAB82212	AAY48056	AAW58064	AAW58063	AAW11019	AAG75172	ADA50560
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45	45	45	45	44	44	44	44	42	41	41	41	41	41	40	40	40	40	40	40
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumuur growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, to treat a cancer spletched from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                            Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215)
                                                                                                                         Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Page 113; 127pp; English
AAE08285 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                    07-FEB-2001; 2001WO-US003977.
                                                                                                                                                                                                                                                                                                                 11-FEB-2000; 2000US-00502600.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                 (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514676/56
                                                                                                                                                                                                                      WO200159158-A1.
                                                                                                                                                                                         Homo sapiens
                                                               01-NOV-2001
                                                                                                                                                                                                                                                     16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                 O'brien TJ;
                                  AAE08285;
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Length 9;

DB 4;

100.0%; Score 50;

Sequence 9 AA;

Query Match

AAB21298

AAU17043

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                  ö
                                                                                                                                                                                                                                                                                                                              immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Aliaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                  Gaps
                    ô
                                                                                                                                                                                                                                                                                                                   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                    Indels
100.0%; Pred. No. 1.4e+06; vative 0; Mismatches 0;
                                                                                                                                                                                 ADA05738 standard; protein; 181 AA
                                                                                                                                                                                                                                                                                     Human NOV18d protein SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0381038P.
2002US-0381042P.
2002US-0381642P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-2002; 2002US-0391335P
01-OCT-2002; 2002US-00262511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002WO-US031373
                                                                                                                                                                                                                                                   (first entry)
     Best Local Similarity 100.
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-03
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                                                                                        GPLVCRGTL 9
                                                        1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003029424-A2.
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05-OCT-2001;
05-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                     ADA05738;
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The present invention describes NoVX proteins, where X can be 1 to 55 cc (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit composition or more containers, the composition described above; (3) an isolated nucleic acid containers, the composition described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (6) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above compression or treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide described above; (10) a method for identifying a potential therapeutic agent for aberrant physiological interactions of the polypeptide (11) a method of a pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the above polypeptide. NoVX or preventing a pathology associated with the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The community appearance and antilipaemic activities, and can be used in gene therapy. The controlled may be used to diagnose, treat or prevent metabolic contents and antilipaemic activities, and can be used in gene therapy. The controlled may be used to diagnose, treat or prevent metabolic content of discorders such as diabetes or obesity, infections, cancer, concerved discorders such as diabetes or obesity, infections, canceris, cancer, in chromosome mapping, issue typing, preventive mentalicine and propes, in chromosome mapp
                                                         New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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0
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                                                                                                                                                                                  Claim 1; Page 171; 586pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA05736 standard; protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
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WPI; 2003-381626/36.
N-PSDB; ADA05737.
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09-0CT-2001; 2001US-03279179.
09-0CT-2001; 2001US-0328029P.
09-0CT-2001; 2001US-0328029P.
09-0CT-2001; 2001US-0328044P.
15-0CT-2001; 2001US-0328449P.
15-0CT-2001; 2001US-034144P.
17-0CT-2001; 2001US-034144P.
18-0CT-2001; 2001US-034162P.
24-0CT-2001; 2001US-034162P.
24-0CT-2001; 2001US-034162P.
24-0CT-2001; 2001US-0341862P.
24-0CT-2001; 2001US-034957P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373814P.
16-MAY-2002; 2002US-0373814P.
                                                                                                                                                                                                                                               29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
                                        02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADA05735
            WO2003029424-A2.
Homo sapiens.
                           10-APR-2003
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(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or

17-APR-2002; 2002US-0373260P

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containt physiological interactions of the polypeptide; (11) a method of acreening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide; nor amanal; and (14) a method for producing the above polypeptide; now account and antidiabetid, ancreating the above polypeptide. Now, sequences have antidiabetid, ancreating, neuroprotective, antiparkinsonian antilipament cativities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic calledrates such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzhaimer's disease or Parkinson's disorders uncleic acids can also used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and processent invantion
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 50; DB 6; Length 198; 100.0%; Pred. No. 1.4; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA05744 standard; protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV18g protein SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-0CT-2001; 2001US-0326483F.
05-0CT-2001; 2001US-032743FP.
09-0CT-2001; 2001US-0327449F.
09-0CT-2001; 2001US-03290-09-0CT-2001; 2001US-032805P.
09-0CT-2001; 2001US-0328056F.
12-0CT-2001; 2001US-0328056F.
15-0CT-2001; 2001US-032814F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2001; 2001US-0341058P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2001; 2001US-0330309P.
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01-NOV-2001; 2001US-0346357P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2002; 2002WO-US031373
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Best Local Similarity luv...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                 present invention.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 198 AA;
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 50; DB 6; Length 224; Best Local Similarity 100.0%; Pred. No. 1.6; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 172; 586pp; English.
19-APR-2002; 2002US-0373817P.

19-APR-2002; 2002US-0373826P.

19-APR-2002; 2002US-0373826P.

22-APR-2002; 2002US-037384P.

16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381038P.

16-MAY-2002; 2002US-0381642P.

17-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0383656P.

29-MAY-2002; 2002US-0383656P.

25-JUN-2002; 2002US-0383656P.

25-JUN-2002; 2002US-0383656P.

25-JUN-2002; 2002US-0383656P.
                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.

Example 10; Fig 1; 130pp; English.

Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain. Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;

(first entry)

03-AUG-2001

AAB98502 standard; protein; 225 AA

**AAB985** 

193 GPLVCRGTL 201

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1 GPLVCRGTL

tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.

20-OCT-2000; 2000WO-US029095.

WO200129056-A1. Homo sapiens.

26-APR-2001.

99US-00421213.

20-OCT-1999;

Tanimoto H;

O'brien TJ,

WPI; 2001-381031/40.

(UYAR-) UNIV ARKANSAS.

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule dascribed above; (3) an isolated nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a pathology that is related to an aberrant expression or use in treating a pathology that is related to an aberrant expression to aberrant physiological interactions of the polypeptide; (11) a method of a citivity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulator of activities described above; (13) method of activities, and carrivity of the polypeptide described above; (13) method of a modulator, cyctostatic, antibacterial, virucide, or mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide is useful in manufacturing a medicament for treating a pathology associated with a hours of an endicament for treating a special in manufacturing a medicament for treating a special in an endicament for treating a special in manufacturing a medicament for treating a special activities, and can be used in gene therapy. The syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to disance, treat or prevent metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 50; DB 4; Length 225; 100.0%; Pred. No. 1.6; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA05742 standard; protein; 247 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 225 AA;
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Best Local 9
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Gaps ö

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human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipsemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                          09-OCT-2001; 200105-0328029P.
09-OCT-2001; 200105-0328044P.
09-OCT-2001; 200105-0328044P.
12-OCT-2001; 200105-0328044P.
17-OCT-2001; 200105-03329414P.
18-OCT-2001; 200105-03304105P.
24-OCT-2001; 200105-0330405P.
24-OCT-2001; 200105-0334265P.
24-OCT-2001; 200105-0334265P.
24-OCT-2001; 200105-0334266P.
17-APR-2002; 200105-0373260P.
19-APR-2002; 200205-037326P.
19-APR-2002; 200205-0373817P.
19-APR-2002; 200205-0373817P.
19-APR-2002; 200205-0373817P.
19-APR-2002; 200205-0373817P.
16-MAY-2002; 200205-0373817P.
16-MAY-2002; 200205-0381032P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
18-MAY-2002; 200205-0381642P.
29-MAY-2002; 200205-0381642P.
                                                                                                                                                        02-OCT-2002; 2002WO-US031373
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                                                                                    Homo sapiens
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25-JUN-2002;
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                                                                                                                                  10-APR-2003
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Eisen AJ,
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG; Shimkets RA, Rochenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

# Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the

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presence or amount of the above polypeptide or nucleic acid molecule in a adhesea associated with altered levels of expression of the above a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide described of greening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide; NoVX sequences have antidabetic, anometric, antibacterial, virucide, immunomodulator, cytostatic, anometric, antibacterial, virucide, immunomodulator, cytostatic, anometric, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antipaxinsonian and antilipaemic activities, and can be used in gene therapy. The cold molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's dispense, immune disorders such as Alzheimer's disease, immune disorders such a shaden and various mapping, tissue typing, preventive medicine and probes, in ohromosome mapping, tissue typing, preventive medicine and present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA05732 standard; protein; 250 AA.
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2001US-0327449P.
2001US-0327917P.
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2001US-0328044P.
2001US-0328056P.
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2001US-0329414P.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 247 AA;
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15-OCT-2001; 2
17-OCT-2001; 2
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05-OCT-2001; 2
09-OCT-2001; 7
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09-OCT-2001; 2
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present invention

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2002US-0373817P
2002US-037384P
2002US-0373844P
2002US-0373844P
2002US-0381037P
2002US-0381042P
2002US-0381042P
   2001US-0341058P.
2001US-0339266P.
2001US-0349575P.
2001US-0346357P.
2001US-0346357P.
2002US-0373815P.
                                                                            2002US-0383656P.
2002US-0383831P.
2002US-0391335P.
                                                                                          2002US-00262511
                                                                                                    (CURA-) CURAGEN CORP.
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N-PSDB; ADA05731.
   22-0CT-2001)
24-0CT-2001)
29-0CT-2001)
29-0CT-2001)
11-NPR-2001)
19-APR-2002)
19-APR-2002)
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16-MAY-2002)
16-MAY-2002)
17-MAY-2002)
28-MAY-2002)
29-MAY-2002)
25-UUN-2002)
                                                                                                                           Ji w, Miller
Shimkets RA,
Eisen AJ, Ga
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

# Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comportsing; in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above adjease associated with altered levels of expression of the above a disease associated with altered levels of expression of the above a disease associated with altered levels of expression of the above a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying an pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of somethod for modulator of activity or of latency or presipposition to a pathology associated with the polypeptide; (12) a method for modulator of activity of the polypeptide described above; (13) method for producing the above polypeptide in a manufacturing a method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a method for producing and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a method for producing and antilipaemic activities, and can be used in gene therapy. The priese such as diabetes or obesity, infections, can be used to diagnose, treat or prevent metabolic displacements in chromosome mapping, issue typing, pheres and such as advanced and a

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                                                                                                                                                                                                                                             human, NOVX, antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                              Gaps
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K, Malyankar UM;
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                     100.0%; Score 50; DB 6; Length 250; 100.0%; Pred. No. 1.8;
                                              0; Indels
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                                             0; Mismatches
                                                                                                                                                    ADA05734 standard; protein; 252 AA
                                                                                                                                                                                                                         Human NOV18b protein SEQ ID NO:94.
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09-0CT-2001; 20010S-0328044P.

12-0CT-2001; 20010S-032814P.

15-0CT-2001; 20010S-032914P.

17-0CT-2001; 20010S-033914P.

18-0CT-2001; 20010S-033914P.

18-0CT-2001; 20010S-031958P.

22-0CT-2001; 20010S-0341058P.

24-0CT-2001; 20010S-034326F.

24-0CT-2001; 20010S-034326F.

29-0CT-2001; 20010S-0343529P.
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2002US-0373826P.
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2001US-0327449P.
2001US-0327917P.
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, Spytek KA,
          Query Match
Best Local Similarity luv...
9, Conservative
                                                                                          204 GPLVCRGTL 212
                                                                    1 GPLVCRGTL 9
Sequence 250 AA;
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Patturajan M,
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callosities; keratosis pilaris; ichthyoses; eczema.

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described and a carrier; (2) at the composition comprising a polypeptide described above and a carrier; (2) at the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell of comprising the nucleic acid molecule described above; (5) a cell of physpetide described above; (5) a cell of presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying a pathology that is related to an aberrant expression or a berrant physiological interactions of the polypeptide; (11) a method of a pathology that is related to an aberrant expression of activity of a pathology associated with the polypeptide; (12) a method for modulator of activity or of latency or predisposition to a pathology associated with the polypeptide described above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide or the nucleic and annilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a pathology associated with the above polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acids and an aborative disorders such as allowed associated with a human disease. The polypeptide or particulation and disease or obesity, inference or polypeptide and sociated with a human disease. The polypeptide or particulation and disease, in chromosome mapping, issue typing, present
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Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Miller CE, Rastelli L, Stone DD, Pena CEA, Shenoy SG; ts RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                     obesity,
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                                                                                                                                                                                           New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obcancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
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                                                                                                                                                                                                                                                                                                                  Claim 1; Page 170; 586pp; English
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(first entry)
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Ort T, Gorma
Ji W, Miller
Shimkets RA,
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09-AUG-1995
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Matches
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The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkratchic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psociasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                               Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amyloid precursor protein protease; Alzheimer's disease, diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 1.8; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amyloid precursor protein protease.
                                                                                                                                                                                                                                                                                                  Disclosure, Page 97; 137pp; English.
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                                                                                               94WO-IB000166.
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                                                                                                                                                (SYMB-) SYMBICOM AB
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                                                                                               20-JUN-1994;
                         Homo sapiens.
                                                                                                                        18-JUN-1993;
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Gaps

us-09-905-083-80.rag

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N-PSDB; AAT39783
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New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.

Claim 1; Page 44-45; 55pp; English.

Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAM39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cpds. useful for treating or develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease

### Sequence 253 AA;

Gaps ö 100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels Ouery Match 100. Best Local Similarity 100. Matches 9; Conservative

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GPLVCRGTL 215 207

### ESULT 11

ABB84421 standard; peptide; 253 AA

#### ABB84421;

(first entry) 08-NOV-2002. Human SCCE protein N-terminal fragment SEQ ID 48.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

### Homo sapiens

WO200262135-A2

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300

09-FBB-2001; 2001CA-02332655. 09-FBB-2001; 2001DK-00000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

Egelrud T, Hansson L;

WPI; 2002-643380/69

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in Skin.

# Example 6; Page 37; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model.

Corrections a pathogenic condition, for development, to relieve or ameliorate a pathogenic condition, for development or testing of a comment or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of an inflammatory skin diseases selected from diseases consisting of epidermal continuity, atopic dermatitis, eczema, acne and inherited skin diseases or prunitus, atopic dermatitis, eczema, acne and inherited skin diseases or with epidermal hyperkratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases compositions compensents the N-terminal compounds and compositions for relieve of various skin diseases compensent of the human stratum corneum chymotryptic enzyme, SCCE transgenic mammals described in the invention 88888888888888888888888

## Sequence 253 AA;

; 0 Gaps ö 100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.

207 GPLVCRGTL 215 Q 1 GPLVCRGTL

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### RESULT 12

ABB84406 standard; protein; 253 AA. ABB84406

#### ABB84406;

08-NOV-2002 (first entry)

## Human SCCE protein.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme. 

WO200262135-A2

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218.

EGELRUD T. HANSSON L. (EGEL/) Egelrud T, Hansson

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WPI; 2002-643380/69.

N-PSDB; ABQ76226

Transgenic mammal or its embryo useful as model for human disease, has hererologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

# Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence

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coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologues acce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or amelioarde a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatities of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum chymotryptic enzyme, SCCE which is a serine procease synonymous with human kallikrein 7 (KLK7) and is used in the development of the
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Sequence 253 AA;

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100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8; tive 0; Mismatches 0; Indels
                                      Conservative
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Best Local Similarity
Matches 9; Conserv
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207 GPLVCRGTL 215

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AAU82740 standard; protein; 253 AA.
            23-APR-2002 (first entry)
        AAU82740;
ESULT 13
  AU82740
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Amino acid sequence of novel human protease #39.

Human, protease, cancer; immune-related disorder; cardiovascular disease, neuronal-associated disease, metabolic disorder; inflammatory disorder; netvous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.

WO200200860-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020171

26-JUN-2000; 2000US-0214047P

(SUGE-) SUGEN INC.

Sudarsanam S, Manning G, Caenepeel S; Whyte D, Charydczak G; Plowman G,

WPI; 2002-139913/18. N-PSDB; ABK31782 Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders

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The present invention relates to the isolation of novel human proteases, and the mucleic acide encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma) cardiovascular diseases (e.g. inflammatory diseases and asthma) cardiovascular diseases (e.g. inflammatory coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. cheumator) attributes and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, usurological disorders (e.g. Alzhaimer's disease, Parkinson's disease) and dyskinesias. The mucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus filly, and non-viral infections such as ocular disease (e.g. human proteases of the invention.
Claim 6; Fig 2N; 313pp; English.
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Sequence 253 AA;

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Gaps
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             100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8;
                                     0; Indels
                                       0; Mismatches
Query Match
Best Local Similarity 100...
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0; Gaps

ABU07440 standard; protein; 253 AA. 28-JAN-2003 (first entry) ABU07440; ABU07440

RESULT 14

Protein differentially regulated in prostate cancer #43:

Prostate cancer, gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring;

WO200281638-A2. 17-OCT-2002, 

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P. 08-APR-2002; 2002WO-US010824.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z,

WPI; 2003-058520/05. N-PSDB; ABX10343 Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises

Page 10

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proseque cancer. (1) is useful for assessing a comprising prostate tissue determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (1) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the polypeptide, and determining whether the test agent modulates the polypeptide, and determining whether the test agent modulates the polypeptide, and determining or treating, assessing, monitoring, prognostication, is useful as molecular markers, as drug targets, and for detecting, products are used in the diagnostic test to assay for presence of cancer. (1) and its expression products are used in the diagnostic test to assay for presence of cancer. e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (1) is useful for assessing cancer e.g., to determine the type discovery. (1) can also be used dea target for therapy or drug discovery. (1) can also be used dea target for therapy or drug discovery. (1) can also be used dea target for therapy or drug discovery. (1) can also be used to restressing the polypeptide and thus functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinically relevant to prostate cancer permits the definitially approach and sequence of a protein differentially and second sequence of a protein differentially applications.
preventive
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Sequence 253 AA;

ò Gaps . 0 DB 6; Length 253; 0; Indels 100.0%; Score 50; DB 6 100.0%; Pred. No. 1.8; Mismatches ö Conservative Query Match Best Local Similarity Matches 9; Conserv

σ 1 GPLVCRGTL

207 GPLVCRGTL 215

ABU07471 standard; protein; 253 AA.

ABU07471;

(first entry) 28-JAN-2003 Protein differentially regulated in prostate cancer #74.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer monitoring

Homo sapiens.

WO200281638-A2.

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z,

WPI; 2003-058520/05. N-PSDB; ABX10375.

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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample comprises the number is indicative of the probability that the sample comprises prostate cancer. (I) is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer. Which involves contentially a prostate cancer in the expression levels in a sample comprising prostate cancer. Or trarget genes which are differentially-regulated in prostate cancer or trarget genes which are differentially-regulated in prostate cancer or translate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent that modulate a biological activity of the polypeptide differentially regulated in prostate cancer cells with a test agents the biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, is useful as molecular markers, as drug targets, and for detecting, is useful as molecular markers, as modulates to disease and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. (The polypeptide endiagnostic test to assay for presence of cancer. (I) as useful for assessing ample, in total Inympy, aspetide encoded by (I) can be used a target for therspy or drug discovery. (I) can also be used for expressing the polypeptide and thus of the polypeptide and thus of the polypeptide and additions to treat prostate cancer. The identification of specific genes, and groups of genes presented in pathways and the delineating or the delineate pathways and the delineating or the delineate or perhways which are
Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                         Claim 1, Page 351; 416pp; English.
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Sequence 253 AA;

Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels

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207 GPLVCRGTL 215 1 GPLVCRGTL 9 ઠે 셤 1, 2004, 17:28:55 Search completed: March Job time : 47,5556 secs

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Sequence 90, Appl
Sequence 498, Appl
Sequence 48, Appl
Sequence 284, Appl
Sequence 742, App
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GenCore version 5.1.6
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US-10-295-027-498
US-09-764-898-284
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14 US-10-106-698-5946 15 US-10-115-479-12 16 US-09-860-739-1 14 US-10-128-966-7 14 US-10-128-966-7 14 US-10-128-966-7 14 US-10-128-966-7 14 US-10-128-966-7 14 US-10-128-966-7 19 US-09-827-946 9 US-09-827-94-10 9 US-09-907-402-1 9 US-09-907-402-1 14 US-10-128-966-1 14 US-10-128-966-1 15 US-10-208-965-1 15 US-10-208-965-1 15 US-10-298-965-1 16 US-10-298-965-1 17 US-10-298-965-1 18 US-10-298-965-1 19 US-09-822-827-947	09-796-294-4
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#### ALIGNMENTS

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RESULT 1
US-09-918-243-80

Sequence 80, Application US/09918243
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Sequence 80, Application US/090142117A1
Sequence 80, Application US/090142117A1
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US-09-905-083-80 ; Sequence 80, Application US/09905083 ; Patent No. US20020146708A1 ; GENERAL INFORMATION:

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CITY: Palo Alto
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Owarian Cancer
FILE REPERRINCE: D6233GIP/C/Div
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: 09/502,600
NUMBER: OF SEQ ID NOS: 136
LENGTH: 9
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OTHER INFORMATION: Residues 207-215 of the SCCE protein
3-09-905-083-80
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TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PLOWNAN, GREGGRY
APPLICANT: PLOWNAN, GREGGRY
APPLICANT: CARREBEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAN, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 036602/1114
CURRENT APPLICATION NUMBER: US/09/886,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR PLING DATE: 2000-06-26
NUMBER OF SEC ID NOS: 150
SOPTWARE: PATENTIN Ver: 2.1
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Patent No. US20020064856A1
GENERAL INFORMATION:
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Matches 9; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
IS-09-888-615-98
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JS-09-764-762-3
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CURRENT MORINA TYPE: Diskete

COMPERATING STRUCK TO WINDOWS VERSION 2.0

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PRICE FILING DATE: 2001-06-18
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-09-764-898-284
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LENGTH: 247
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                                                                                                                                                GERERAL INCREMATION
GENERAL Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Richard
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Matson, Susan R.
CURREMY FILING DATE: 2002-11-13
RRIOR PRICK PLING DATE: 2001-11-13
RRIOR PLING DATE: 2001-11-15
RRIOR PLING DATE: 2001-10-10
RRIOR PLING DATE: 2002-01-10
RRIOR PLING DATE: 2002-01-10
RRIOR PLING DATE: 2002-01-10
RRIOR PLING DATE: 2002-01-10
RRIOR PLING DATE: 2002-02-13
RRIOR PLING DATE: 2002-
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Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurf C.
APPLICANT: Gish, Kurf C.
APPLICANT: Dos Blotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian TITLE OF INVENTION: Cancer FILE REFERENCE: 018501-002420US
CURRENT FAPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
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100.0%; Score 50; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                               Sequence 498, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
JS-10-295-027-498
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       SULT 6
-10-295-027-498
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RESULT 11
US-10-055-569A-69
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: misc feature
LOCATION: (1477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (201)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
JS-10-092-1S4-742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids MAMB/KEY: SITE 100 STR 100 
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CIHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 5-09-764-847-742
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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S-10-092-154-742.
S-10-092-154-742.
Publication Vo. US20030054375A1
GENERAL INFORMATION:
APPLICANT: ROSE of al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION Nucleic No/10/092,154
CURRENT APPLICATION NURBER: US/10/092,154
CURRENT FILING DATE: 2002-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: ParentIn Ver. 2.0
SEQ ID NO 742
LENGTH: 247
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
PAIGE OF SEQ. ID NOS: 2003
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 742
LENGTH: 247
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90.0%; Score 45; DB 9; Length 247;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels
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LOCATION: (145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (148)
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APPLICANT: Padigaru, Muraltudara
APPLICANT: Taugier Jr., Raymond J
APPLICANT: Taugier Jr., Raymond J
APPLICANT: Taugier Jr., Raymond J
TITLE OF INVENTION No. USCO4002418Alal Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION No. USCO4002418Alal Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION No. USCO400404
TITLE REPERENCE: 21402-191
CURRENT FILING DATE: 2001-10-26
PRIOR PELICATION NUMBER: 60/243,642
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR PELICATION NUMBER: 60/243,592
PRIOR FILING DATE: 2000-10-26
PRIOR PELICATION NUMBER: 60/243,681
PRIOR APPLICATION NUMBER: 60/243,983
PRIOR FILING DATE: 2000-11-0.
PRIOR PELING DATE: 2000-11-0.
PRIOR PELING DATE: 2000-11-0.
PRIOR FILING DATE: 2000-11-0.
PRIOR PELING DATE: 2000-11-0.
PRIOR FILING DATE: 2000-11-0.
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Query Match 90.0%; Score 45; DB 14; Length 247; Best Local Similarity 88.9%; Pred. No. 3.9; Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 69, Application US/10055569A Publication No. US20040024181A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellerman, Karen
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gangolli, Esha A
Spytek, Kimberly A
Gilbert, Jennifer
Gaman, Stacie
Blalock, Angela
Li, Li
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Gerlach, Valerie L
Edinger, Shlomit
Malyanker, Uriel
Stone, David
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Gunther, Erik
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Best Local Similarity 88.9<sup>5</sup>
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-055-569A-69
                                                                                                                                       1 GPLVCRGTL 9
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PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-10-31

PRIOR PELING DATE: 2000-10-31

PRIOR PELING DATE: 2000-11-31

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR PILING DATE: 2000-11-01

PRIOR PILING DATE: 2000-11-02

PRIOR PELING DATE: 2000-11-02

PRIOR PELING DATE: 2000-11-02

PRIOR PILING DATE: 2000-11-02
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GPLVCNGSL 212
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APPLICANT Millet, David
APPLICANT Gunther, Elsebale
APPLICANT Gunther, Elsebale
APPLICANT Gunther, Elseman, Glennda
APPLICANT Gunther, Elseman, Maraidhara
APPLICANT Taupier O'I. Raymond J
APPLICANT TAUDier O'I. Raymond J
APPLICANT Anderson, David W
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 21402-191
CURENT APPLICATION NUMBER: US/10/055,569A
CURRENT APPLICATION NUMBER: 60/243,642
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR PLLING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,320
PRIOR PLLING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,592
PRIOR APPLICATION NUMBER: 60/243,592
PRIOR PILING DATE: 2000-10-26
PRIOR PILING DATE: 2000-10-26
PRIOR PILING DATE: 2000-10-27
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                                                                                                                                                                             Sequence 212, Application US/09764898
Patent No. US200200573A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ01 NUMBER: US/09/764,898
CURRENT APPLICATION UNDER: US/09/764,898
CURRENT APPLICATION DATE: 2011-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 212
LENGTH: 251
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Publication No. US20040024181A1
GENERAL INFORMATION:
APPLICANT: Gangolli, Esha A
APPLICANT: Spytek, Kimberly A
APPLICANT: Gibert, Jennifer
APPLICANT: Galbert, Jennifer
APPLICANT: Hallock, Angela
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Gerlach, Valerie L
Edinger, Shlomit
Malyanker, Uriel
Stone, David
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Vernet, Corine
Shenoy, Suresh
Mishra, Vishnu S
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                                                                    206 GPLVCNGTL 214
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S-09-764-898-212
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                  1 GPLVCRGTL 9
                                                                                                                                                                3-09-764-898-212
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Sequence 5, Application US/09860739
Sequence 5, Application US/09860739
Publication No. US20030166036A1
GENERAL INFORMATION:
Publication No. US20030166036A1
GENERAL INFORMATION:
Processe and an Aminopeptidase Associated with Development of B TITLE OF INVENTION: A processe and an Aminopeptidase Associated with Development of B TITLE OF INVENTION: Processe and Aminopeptidase Associated with Development of B TITLE OF INVENTION: Development of B TITLE OF 
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Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps
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PRIOR APPLICATION NUMBER: 60/245,029
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,995
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/245,293
PRIOR FILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 276
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80.0%; Score 40; DB 10; Length 54;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels
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Tob time : 24.1111 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
}-10-055-569A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Homo sapiens S-09-860-739-5
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S-09-860-739-5
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein - pr	protein - protein search, using sw model
m on:	March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec
.tle: arfect score: aquence:	US-09-905-083-80 50 TOLVCRGTL 9
oring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5

otal number of hits satisfying chosen parameters: 28

283366 segs, 96191526 residues

sarched:

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Maximum Match 100%
Listing first 45 summaries

Listing first 45: PIR\_78:\*

atabase : PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	serine proteinase	semenogelase (EC 3	tissue kallikrein	probable aminoglyc		tissue kallikrein	complement factor	semenogelase (EC 3	glandular kallikre	tissue kallikrein	sene	ka]	ğ	obable ser	kallikrei	(EC 3	Œ	call:	kallikrein, glandu	psi	1	tonin (EC 3.4.21	kall	tissue kallikrein	sin -	tissue kallikrein	nerve gro	ssue kalli	tissue kallikrein
		ΩI	A53968	A32297	A29586	T35999	G72548	KORTP	DBHU	835711	I49416	A05308	515395	B23863	B32340	S45356	A27207	S39047	S39048	A44284	S15685	S35585	I56220	KORTIN	D23863	A29746	I56559	KQMS1	NGMSG	TRMSMS	A34079
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		Match Length	253	261	261	262	155	265	246	261	46	96	104	156	188	225	239	240	241	244	250	254	258	259	259	259	260	261	261	261	261
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	esult	No.		N	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

tissue kallikrein	gamma-renin (EC 3.	tissue kallikrein	tissue kallikrein		tissue kallikrein	granzyme 3 (EC 3.4	riboflavin biosynt	kallikrein - mouse	elastase (EC 3.4.2	tissue kallikrein	duodenase - bovine	~	_	trypsin (EC 3.4.21	snake venom factor
176108	A28062	A25606	A29745	845303	S15686	565663	T12994	I52972	S44462	KOMSM	569370	TRDFS	TRPGTR	531778	A32121
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261	261	261	261	261	263	264	599	99	73	149	226	229	231	231	236
74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0
37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	4 0	41	42	43	44	45

#### ALIGNMEN

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semenogelase (EC 3.4.21.77) precursor [validated] - human
NyAlternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate.
C;Species: Homo saptens (man)
C;Date: 19-may-2000 #sequence revision 19-May-2000 #text change 08-Dec-2000
C;Accession: A32297; A32423; S03604; S05468; S05467; A32546; S02239; A26757; C31567; A31:
R;Riegman, P.H.J.; Vileterra, R.J.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
B;Dobhwa. Biophys. Res. Commun. 159, 95-102, 1989
A;Title: Characterization of the prostate-specific antigen gene: a novel human kallikren:
A;Accession: A32297; MUID:89165891; PMID:2466464
A;Accession: A32297; MUID:89165891; PMID:2466464
A;Accession: A32297
A;Status: preliminary
A;Residues: 1-261 <RIE>
A;Cross-references: GB:M24543
A;Residues: 1-261 <RIE>
A;Cross-references: GB:M24543
A;Reiduea: Biophys: Res. Commun. 161, 1151-1159, 1989
A;Title: Characterization of the gene for prostate-specific antigen, a human glandular k, A;Reference number: A32423; MUID:89302090; PMID:2472789
                                                                                                                                                                                                                R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. J. Biol. Chem. 269, 19420-19426, 1994
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Clohing, expression, and characterization of stratum corneum chymotryptic enzym. A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
serine proteinase SCCE precursor - human
N'Alternate names: stratum corneum chymotryptic enzyme
C'Species: Homo sapiens (man)
C'Date: 07-Jul.1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C'Accession: AS3968
                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Status: preliminary
A;Molecule type: mENA
A;Molecule type: mENA
A;Residues: 1-253 < HAN>
A;Residues: 1-253 < HAN>
A;Cross-references: GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 100.0%; Score 50; DB 2; Length 253; Local Similarity 100.0%; Pred. No. 0.085; los 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7435-7435
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GPLVCRGTL 215
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Accession: \$03604 Molecule type: DNA Residues: 1-261 <DIG> Cross-references: EMBL:X13940

Cross-references: EMBL:X14810

Accession: A32546

Molecule type: DNA Residues: 1-29 <KL2>

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A,Accession: 800232; MULDIBBO82800; FMID:3591515
A,Accession: 800232
A,Accession: 800232
A,Readuse: 25-361 -8C2>
A,Readuse: 25-361 -8C2>
A,Readuse: 25-361 -8C2>
B,Watt, X.W.X.; Lee, P.J.; W.Timkulu, T.; Chan, W.P.; Loor, R.
B,Accession: Mall Acad. Sci. U.S.A. 83, 3166-3170, 1996
A,Attle: Human prostate-specific antigen: structural and functional similarity with serin
A,Accession: A23937
A,Molecule type: protein
A,Residues: 25-93,77,95-164,411,166,7DQM',169-174,0',176-261 <AAT>
A,Accession: G01551
A,Beference number: G07735
A,Accession: G01551
A,Beference number: G07735
A,Accession: G01551
A,Beference number: G07735
A,Accession: G01551
A,Beference number: BMB:U17040; NID:9595945; PIDN:AAA56764.1; PID:9595946
A,Accession: G07735

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C;Species: Homo sapiens (man)
C;Accession: A29586
R;Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
DNA 6, 429-437, 1987
A;Title: Primary structure of a human glandular kallikrein gene.
A;Title: Primary structure of a human glandular kallikrein gene.
A;Reference number: A29586; MUID:88054467; PMID:2824146
A;Reference 1-type: DNA
A;Residues: 1-261 <2GHs
A;Residues: 1-261 <2GHs
A;Cross-references: GB:MI8157; NID:g186640; PIDN:AAA74454.1; PID:g386842
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A/Molecule type: protein.
A/Accession: S41212
A/Molecule type: protein.
A/Rocession: S41212
A/Rocession: S41212
A/Rocession: S1212
A/Rocession: S1212
A/Genetics: S1213
A/Ge
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             A; Reference number: S00232; MUID:88082806; PMID:3691515
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Matches 7; Conservative
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4, Cross-references: GB:M21897, NID:g189529; PIDN:AAA59997.1; PID:g189530
4, Note: the authors translated the codon GGC for residue 28 as Arg, TGG for residue 29 a 3, Schaller, J.; Akiyama, K.; Tsuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
3ur. J. Biochem. 170, 111-120, 1987
4, Title: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a 9
Accession: A32423
Status is preliminary
Molecule type: DNA
Residues: 1-261 < LUNA
Cross-references: GBNA27274; NID:g190552; PIDN:AAA60192.1; PID:g190553
DAGDY, M.; Zhang, X.Y.; Richards, R.I.
Toleic Acids Res. 17, 2137, 1989
Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
Reference number: 803604; MUID:89183612; PMID:2467258
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"Readues: 1-72,"T',74-85,"I',87-174,"P',176-183,"Q',185-259,"D',261 <HEN>
"Scalerences: GB:M2663

"Schulz, P.; Stucka, R.; Feldmann, H.; Combriato, G.; Klobeck, H.G.; Fittler, F.
uclaic Acids Res. 16, 6226, 1988

"Titler: Sequence of a cDNA clone encompassing the complete mature human prostate specifices and prostate specifices in S02239; MUID:88289366; PMID:2456523
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N;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
N;Accession: A31567
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1;Residues: 5-210, WVILITELIMPA',223,'PMVIHGSLV',233,'WRGGV' <RI3>
4;Croserreferences: GB:M21896; NID:g189525; PIDN:AAA59996.1; PID:g189526
4;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
4;Accession: B31567
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"Residues: 5-261 <LU2>

"Rategman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.

"Stategman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.

Siochem. Biophys. Res. Commun. 155, 181-188, 1988

Nochem. Biophys. Res. Commun. 155, 181-188, 1988

Nochem. Biophys. Res. Commun. 155, 181-188, 1988

N.T. Trile: Molecular cloning and characterization of novel prostate antigen cDNA's.

N.Reference number: A90144, MUID:88326297; PMID:2458104
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:Molecule type: DNA
:Molecule type: DNA
:Keaduses: 1-261 (KLI)
:Cross-treferences: EMBL:X14810; NID:g35732; PIDN:CAA32915.1; PID:g296671
:Cross-treferences: EMBL:X14810; NID:g35732; PIDN:CAA32915.1; PID:g296671
:Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
:Alobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
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./Residues: 17-63, Tr',65-135,'M',137-261 <SCH>
./Crose-references: EMB:X07730
./Lundwall, A.; Lilja, H.
EMB Lett. 214, 317-322, 1987
./Title: Molecular clouing of human prostate specific antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, immitted to the EMBL Data Library, May 1989
Reference number: S05468
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1; Molecule type: mRNA 1; Residues: 5-261 <RI2>

1, Accession: C31567

1;Accession: A26757

A, Molecule type: mRNA

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Lissue kallikrein (BC 3.4.21.35) precursor - rat
N;Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
N;Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Morway rat)
C;Date: 05-Apr-1983 #sequence revision 05-Apr-1983 #text change 16-Jun-2000
C;Accession: A00944; A41429; A25137; JX0073; A23863; A3339
R;Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Title: Rat pancreatic kallikrein mRNA: nucleocitde sequence and amino acid sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
,Residues: 115-265 «GER»
;Inoue, H.; Fukul, K.; Miyake, Y.
= Biochen, H.; Fukul, K.; 1989
= Biochen 105, 834-840, 1989
;Ittle: Identification and structure of the rat true tissue kallikrein gene expressed in
;Reference number: JX0073; MUID:89327211; PMID:2753879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-265 <SWI>
A,Experimental source: pancreatic
A,Experimental source: pancreatic
A,Experimental source: pancreatic
J, S, S, Managa, S.
J, Blochem. 102, 1389-1404, 1987.
A,Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit A,Reference number: A41429; MUID:88198057; PMID:3482210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Status: preliminary
A.Molecule type: protein
A.Molecule type: protein
R.Gerald, W.L.; Chao, J.; Chao, L.
B.Gerald, W.L.; Chao, J.; Chao, L.
B.Jochim. B.Lophya: Acta 866, 1144, 1986
A.Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A.Reference number: A25137; MUID:86131678; PMID:3004582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashley, P.L.; MacDonald, R.J.
iochemistry 24, 4512-4520, 1985
.Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
?Reference number: A22863; MUID:86051477; PMID:2998455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: submaxillary gland
R; Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
Biol. Chem. 264, 7653-7662, 1989
A; Title: Organization and expression of the rat kallikrein gene family.
A; Reference number: A33359; WUID:89214217; PMID:2708383
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;Cross-references: GB:D00448; NID:g220792; PIDN:BAA00346.1; PID:g220794
;Experimental source: kidney
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C;Comment: Tissue kallikreins cleave
C;Genetics:
A;Introns: 20/1; 73/2; 169/1; 214/3
C;Superfamily: trypsin, trypsin home
C;Keywords: hydrolase; pancreas; sea
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A,Molecule type: DNA
A,Residner
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2, Kawarabayasi, Y.; Hino, Y.; Hozikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
wa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; R
NA Res. 6, 83.101, 1999
4, Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
4, Reference number: A72450; MUID:99310339; PMID:10382966
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A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: EMBL:AL096839; PIDN:CAB50752.1; GSPDB:GN00070; SCOEDB:SCC22.09; Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cobable aminoglycoside acetyltransferase - Streptomyces coelicolor species: Streptomyces coelicolor bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
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;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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Note: the authors translated the codon TAC for residue 43 as Trp Genetics:
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80.0%; Score 40; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 2; Indels
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                                                          Introis: 16/1; 69/2; 165/1; 210/3
Superfamily: trypsin; trypsin homology
Keywords: hydrolase; serine proteinase
25-253/Domain: trypsin homology cTRY>
65,120,213/Active site: His, Asp, Ser #status predicted
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Best Local Similarity 88.5%
Conservative
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ACESON Fisher Allikrein (EC 3.4.21.35), submandibular mCK-2 - mouse (fragment)
NyAlternate names: glandular kallikrein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: ACESON
R;Accession: ACESON
R;Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.
A;Title: Structure of mouse kallikrein gene family suggests a role in specific processing
A;Reference number: A00941; MUID:83219214; PMID:6602295
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A;Residues: 1.96 <MAS>
A;Cross-references: GB:V00829; NID:g52775; PIDN:CAA24212.1; PID:g388523
A;Cross-rimental source: Quakenbush inbred strain
A;Rxper-imental source: Quakenbush inbred strain
A;Note: this sequence has been translated from two exons (11-147 and 522-674) located ups
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
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Jahldur kallikrein - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: 149416
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
A;Accession: 149416
A;Accession: Jay416
A;
                                                      Cypercession, Macan mistage revision 19-May-2000 #text_change 19-May-2000 Cypercession, 535711, 534219

Rydauthier, E.N. Chapdelaine, P.; Temblay, R.R.; Dube, J.Y.

Rydauthier, E.N. Chapdelaine, P.; Temblay, R.R.; Dube, J.Y.

Blochim. Biophys. Acta 1174, 207-210, 1993

A,Title: Characterization of rhesus monkey prostate specific antigen cDNA.

A,Reference number: 535711; MUID:93363642; PMID:7689340

A,Recession: S35711

A,Molecule type: mRNA

A,Residues: 1-261 cGAU>

A,Cross-references: ENBL:X73560; NID:9311843; PIDN:CAA51957.1; PID:9311844

C,Comment: This enzyme preferentially cleaves after tyrosine residues.

C,Comment: This enzyme preferentially cleaves after tyrosine residues.

C,Superfamily: trypsin homology

C,Keywords: 91ycoprotein; hydrolase; prostate; serine proteinase

F;18-24Domain: propeptide #status predicted cRCO>

F;25-261/Product: semenogelase #status predicted cNGO>

F;25-261/Product: rypsin homology <TRY>
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Pred. No. 14;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F)25-253/Domain: trypsin homology <TRY>F;65,120,213/Active site: His, Asp, Ser #status predicted
                    Species: Macaca mulatta (rhesus macaque)
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Best Local Similarity 77.8%;
Matches 7; Conservative
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es 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mplement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
Alternate names: adipsin; C3 convertase activator
Species: Home sapiens (man)
Date: 28-Aug-1985 #sequence revision 31-Dec-1992 #text_change 08-Dec-2000
Accession: A40197; A00936; A60571; S66645
White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;
Biol. Chem. 267, 9210-9213, 1992
Title: Human adipsin is identical to complement factor D and is expressed at high leve Reference number: A40197; MUD:92250520; PMID:1374388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       semenogelase (EC.3.4.21.77) precursor - rhesus macaque N; Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate \delta
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.,Status: preliminary
.,Molecule type: protesin
.,Residues: 19-44, C',46-48 <BAL>
.;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
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Superfamily: trypsin; trypsin homology

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:Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
iochemistry 23, 2482-2486, 1984
;Title: Amino acid sequence of human D of the alternative complement pathway.
Reference number: A00936; MUID:85000441; PMID:6383466
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             78.0%; Score 39; DB 1; Length 265; 66.7%; Pred. No. 9.4; 2; Indels ative 1; Mismatches 2; Indels
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76.0%; Score 38; DB 1; Length 246;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels
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Query Match
Sest Local Similarity 66.79
Matches 6; Conservative
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Residues: 1-246 <WHI>
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C;Accession: B32340
R;Shai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
Richai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
A;Dichemistry 28, 5334-5343, 1989
A;Title: Characterization of genes encoding rat tonin and a kallikrein-like serine prote A;Reference number: A32340; MUID:89375248; PMID:2550051
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-188 <SHA>
A;Cross.references: GB:NZ6534; NID:g206773; PIDN:AAA42080.1; PID:g206774; GB:J02860
C;Superfamily: trypsin, trypsin homology
C;Reywords: hydrolase; serine proteinase
F;1-180/Domain: trypsin homology (fragment) <TRY>
                                                                    tissue kallikrein (EC 3.4.21.35) 3 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
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Altlernate names: glandular kallikrein
C;Species: Cavia porcellus (guinea pig)
C;Date: 08-Mar-1289 #sequence_revision 08-Mar-1989 #text_change 01-Aug-1997
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A;Experimental source: Alzheimer's disease patient brain cortex
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C,Accession: 845356
E,C,Dhanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A,Title: A novel serine proteinase-like sequence from human brain.
A,Reference number: 845356; MUID:94289486; PMID:8018728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.0%; Score 37; DB 2; Length 188; Best Local Similarity 66.7%; Pred. No. 16; Matches 6; Conservative 1; Mismatches 2; Indels
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Biochemistry 26, 3471-3478, 1987
A;Title: Amino acid sequence of guinea pig prostate kallikrein.
A;Reference number: A27207; MUID:88000549; PMID:3307909
A;Accession: A27207
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Matches 7; Conservative
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142 GPLICDGVL 150
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A; Residues: 1-225 < DIH>
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A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        issue kallikrein-related proteinase (EC 3.4.21.-) k10 - rat (fragments)
;Species: Rattus norvegicus (Norway rat)
;Saceies: Rattus norvegicus (Norway rat)
;Aate: 18-Feb-1994 #sequence_revision 19-Jul-1996 #text_change 17-Oct-1997
;Aate: 18-Feb-1995; S1548
R;Gutman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F.
aur. J. Biochem. 197, 425-429, 1991
A;Ritle: Microheterogeneity of rat submaxillary gland kallikrein k10, a member of the ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fil-104/Domain: trypsin homology (fragments) <TRY>
Fil-204/Domain: trypsin homology (fragments) <FI-23/Product: tissue kallikrein-related protein k10 light chain (fragment) #status exp Fig-51-57/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex Fi52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex Fi52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex Fi52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex Fi52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment)
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Jochemistry 24, 4512-820, 1985
Title: Kalikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
Reference number: A23863; MUID:86051477; PMID:2998455
                                  .;Introns: 45/3
;Superfamily: trypsin; trypsin homology
;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
;1-88/bomain: trypsin homology (fragment) <TRY>
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NiAlternate names: glandular kallikrein; kininogenin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 22-Jun-1999
C;Accession: B23863
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A) Cross-references: GB:M11564; NID:9205031; PIDN:AAA41465.1; PID:9205032
C) Superfamily: trypsin, trypsin homology
C) Keywords: hydrolase; serine proteinase
F)1-148/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 37; DB 2; Length 156; 66.7%; Pred. No. 14; ative 1; Mismatches 2; Indels
                                                                                                                                                                                                        74.0%; Score 37; DB 2; Length 96; larity 66.7%; Pred. No. 8.8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: protein
A, Residues: 1.23:24-51;52-104 <GUT>
A, Experimental source: submaxillary gland
C, Superfamily: trypabin, trypabin homology
C; Keywords: hydrolase; serine proteinase
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Best Local Similarity 66...
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                                                                                                                                                                                                                                           Best Local Similarity
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A; Residues: 1-156 <ASE
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Map position: 7
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Gaps . 0

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Residues: 1-239 <DUN>
Note: 50-Trp was also found
Superfamily: trypsin, trypsin homology
Keywords: hydrolase; serine proteinase
1-231/Domain: trypsin homology <TRY>
41,96,191/Active site: His, Asp, Ser #status predicted
```

0; Gaps Query Match 74.0%; Score 37; DB 2; Length 239; Best Local Similarity 66.7%; Pred. No. 20; Matches 6; Conservative 1; Mismatches 2; Indels

1 GPLVCRGTL 9 |||:||| 193 GPLICDGVL 201

Parch completed: March 1, 2004, 17:36:31 b time : 11.3333 secs

us-09-905-083-80.rpr

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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| protein - protein search, using sw model

March 1, 2004, 17:17:25 ; Search time 6 Seconds (without alignments) 78.105 Million cell updates/sec n on:

tle: rfect score:

US-09-905-083-80 50 1 GPLVCRGTL 9 :dnence:

Gapop 10.0 , Gapext 0.5 oring table: BLOSUM62

141681 seqs, 52070155 residues sarched:

141681 stal number of hits satisfying chosen parameters:

inimum DB seq length: 0 aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_42:\* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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KLK3, MOUSE KLK5, MOUSE KLK8, RAT KLK8, RAT KLK9, MOUSE KLK9, MOUSE KLKG, MOUSE KLK7, PRANA GRAK, HUMAN GRAK, HUMAN GRAK, HUMAN	
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#### ALIGNMENTS

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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-25, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

--- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

---- SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.

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                                                                                                                                                                                   16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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                                                                                                                                                                                                                                                                                              GO: GO:0008236; F:serine-type peptidase activity; TAS.
GO: GO:0008544; P:epidermal differentiation; TAS.
InterPro; IPR001303; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase SlA.
InterPro; IPR001314; Peptidase SlA.
Ffam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMCIRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00200; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN INS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease; Zymogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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KALLIKREIN 7.
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                                                                                                                                                                                          EMBL, L33404; AAC37551.1; -.
EMBL, AR16530; AAL49718.1; -.
EMBL, AR24527; AAC33360.1; -.
EMBL, AF332583; AAK69624.1; -.
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                                                                                                                                                                                                                                       PIR, A53968, A53968.
HSSP, P00763, IDPO.
MEROPS, S01.300, -.
Genew, HGNC:6368; KLK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
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253 AA;
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KLK9 HUMAN
1D 7LK9 HUMAN
AC 09UK09;
DT 16-0CT-2001
DT 28-FEB-2003
DE KAllikrein 9
DE L3).
GN KLK9.
CS HUMAN
CS KLK9.
CS EUKALYOCA; M
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Danganan L., Stler A., Christensen M., Georgescu A., Brower A., Garnes J.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.,

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUB SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20247258; PubMed=10783266;
Yousef G.M., Diamandis E.P.;
"The expanded human kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3.";
Genomics 65:184-194(2000).
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                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINES-20118156, PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis B.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PÖTENTIAL.
KALLIKREIN 9.
CHARGE RELAY SYSTEM (BY SIMILABITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
Gene 257:119-130 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R WBL; AP243527; AAG33362.1; -
R WBL; AP243527; AAG33362.1; -
R WBRD; AC01143; AAG32255.1; -
R WBRCPS; SO1.307; --
R GARW; HGNC; G370; KLK9.
R GG; GO:0005576; C:extracellular; NAS.
GG; GO:0005576; C:extracellular; NAS.
GG; GO:0005576; C:extracellular; NAS.
R GG; GO:0005509; P:proteclywis and peptidolysis; NAS.
R InterPro; IPRO10254; Peptidase_81.
R InterPro; IPRO10254; Peptidase_81.
R InterPro; IPRO10254; Peptidase_81.
R PRINTS; PRO1025; CHYMOTRYPEIN.
R PRINTS; PRO1025; CHYMOTRYPEIN.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN JES; 1.
R PROSITE; PS00134; TRYPSIN JES; 1.
R PROSITE; PS00134; TRYPSIN JES; 1.
R PROSITE; PS00135; TRYPSIN JES; 1.
R PACATASIN JES; 1.
R PROSITE; PS00135; TRYPSIN JES; 1.
R PACATASIN JES & DATE ADAPMENT AND ADAPME
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999).
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Burkhart-Schultz K., Gordon L., Raglal W., Raintez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amito-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and characterization of KLK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."; Genomics 73:117-122(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yousef G.M., Diamandis E.P., "Modecular Characterization," mapping, and tissue expression of KLKL6, a hormonally regulated Rallikrein-like gene."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.
MEDLINE=20545474; PubMed=10969073;
Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K., Clements J.A.;
"Tissue-specific expression patterns and fine mapping of the human
                                                                                                                                                                                        Gaps
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kallikrein (KLK) locus on proximal 19q13.4.";
J. Biol. Chem. 275:37397-37406 (2000).
-!- SUBCRILULMAR LOCATION' Secreted (Probable).
-!- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen,
                                                                                                                                                                                                                                                                                                                                                                                                  KLXKA OR KLXL6.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Kallikrein 14 precursor (BC 3.4.21.-) (Kallikrein-like protein 6)
                                                                                                                                                                                        ö
                                                                                                                                                           90.0%; Score 45; DB 1; Length 250; 88.9%; Pred, No. 0.16; 1; Indels cive 0; Mismatches 1; Indels
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Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A.,
Ashworth L.K., Clements J.A.;
                                                                                                                                                                                        1; Indels
                                                                                                                                    27512 MW; F2785245B063E98B CRC64;
                                                                                                                                                                                                                                                                                                            PRT; 251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                         Local Similarity 88.9
nes 8; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                         206 GPLVCNGTL 214
                                                                                                                                                                                                                 1 GPLVCRGTL 9
                                                                                            131
166
211
250 AA;
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                               -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Venom serine proteinase A precursor (BC 3.4.21,-).
Bothrops jararaca (Jararaca).
Bothrops jararaca (Jordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Thrombin-like snake venom serine protease.
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prostate and skeletal muscle
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251 AA;
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TISSUE=Venom gland;
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VSP3_BOTJA
ID__VSP3_BOTJA
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are or restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuropsin precursor (BC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
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KLK8 OR PRSS19 OR NRPN OR BSP1.
                                                                                                                                                                                                                               EMBL; AB031394; BAA89310.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Fischer; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 75.0 les 6; Conservative
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206 GPLICNGT 213
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TREAT
TO 088780;
TO 15-070-199
TT 15-070-199
TT 28-FEB-20(
DE Neuropsin
DE POOCEASE
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Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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RESOPS (02.13-2).

REPORT (02.13-2).

REPORT (02.13-2).

REPORT (02.13-4).

REPORT (03.13-4).

REPORT (03.13
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WEDLINE-228825; Pubmed-12477932;

REDLINE-228825; Pubmed-12477932;

RIABBER R.D., Collins F.S., Hagner L., Shenmen C.M., Schuler G.D.,

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Bosak S.A., McEwan P.J., McKernan K.J., Ahramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Raha S.S., Collin W. Sodergren E.J., Dickson M.C.,

Raha S. S., McMan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raha S. S., Shelin J.E., Jones S.J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Robriguez A.C., Grimwood J., Schmutz J., Myarra M.A.,

Robriguez C.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Robriguez C.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Robriguez C.M., Krzywinski M.I., Marra M.A.,

Robriguez C.M., Maganeroses M., Maganeros
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
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Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99318093, PubMed=10391209,
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lahe C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
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Lander E.S.;
                                                                                                                                                                                                                                                                                         "Identification and androgen-regulated expression of two major human glandular kallikrein-1 (hGK-1) mRNA species."; Mol. Cell. Endocrinol. 76:181-190(1991).
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MEDILINE=20510930; PubMed=11054574;
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Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
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cluster located in chromosome 19q13 region.";
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TISSUB=Prostate;
TISSUB=1726490;
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Trapman J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
MEDLINE=88054467; PubMed=2824146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
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GDSGGPLVCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRK
                                                                                                                                                                                                                                                 in kininogen to release Lys-bradykinin.
-!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in small molecule substrates. Highly selective action to release kalidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P20151-3; Sequence=VSP_005400;
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYBIN.
PROSTITS; PS00205; TryP_SPC; 1.
PROSTITS; PS00134; TryPSIN_NIS; 1.
PROSTITS; PS00135; TRYPSIN_NIS; 1.
Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen; Signal; Alternative splicing; Polymorphism.
1 18 PR08ABLE.
                                                                           Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                            Nat. Genet. 23:373-373(1999).
-!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION PEPTIDE (PROBABLE).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0004293; F:tissue kallikrein activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing, Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P20151-1; Sequence=Displayed;
Name=2; Synonyms=PGK-10A;
IsoId=P20151-2; Sequence=VSP_005399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF188745; AAF08275.1; -.
AF188746; AAF08276.1; -.
AF188747; AAF08277.1; -.
AF243527; AAG33356.1; -.
AC037199; -; NOT ANNOTATED CDS.
BC005196; AAH05196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M18156; -; NOT_ANNOTATED_CDS.
EMBL; M18157; AAA7454.1; -.
EMBL; S39329; AAD13816.1; -.
EMBL; S39329; AAD13816.1; -.
Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A29586; A29586.
HSSP; P07288; IPFA.
MEROPS; S01.161; ..
Genew; HGNC:6363; KLKZ.
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A RETTT BETTT BETTT BETTT BETTT BETTT BETTT BETT BETT BETTT BETTT BETTT BETTT BETTT BETTT BETTT BETTT BETTT BE
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P07288; 0L672;
01-APR-1988 (Rel. 07, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostate specific antigen precursor (RC 3.4.21.77) (PSA) (Gammaseminoprotein) (Kallikrein 3) (Semenogelase) (Seminin) (P-30 antigen).
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89183632; PubMed=2467258; Digby M.R., Zhang X.Y., Richard R.I.; Milman prostate specific antigen (PSA) gene: structure and linkage to the kallikrain-like gene, hGK-1."; Nucleic Acids Res. 17:2137-2137 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kundwall A.;
cundwall A.;
cundwall A.;
WIKDTIAANP -> VSHPYSQHLEGK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89246551; PubMed=2470373; Henttu P., Vihko P.; For the entire human prostate specific antigen shows icDNA coding for the entire human prostate specific antigen shows high homologies to the human tissue Kalikrein genes."; Biochem. Biophys. Res. Commun. 160:903-910(1989).
                                                                                                                                                                                                                                                                                                                Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                  ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klobeck H.-G., Combriato G., Schulz P., Arbusow V., Fittler F.; "Genomic sequence of human prostate specific antigen (PSA)."; Nucleic Acids Res. 17:3981-3981(1989).
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"Molecular cloning of human prostate specific antigen cDNA.";
FEBS Lett. 214:317-322(1987).
                                                                                              Score 40; DB 1; Length 261;
                                                                                                                   2; Indels
                 /Frid=VSP 005399.
Missing (In isoform 3).
/Frid=VSP 005400.
V -> L (In dbSNP:6072).
/Frid=YSR 014164.
W; 9CFFF4AII62EF42D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glandular kallikrein.";
Biochem. Biophys. Res. Commun. 161:1151-1159(1989).
                                                                                                         Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Leukocyte;
MEDLINE=89302090; PubMed=2472789;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89282407; PubMed=2471958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87190978; PubMed=2436946;
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MEDLINE=89165891; PubMed=2466464;
                                                                        261 AA; 28671 MW;
                                                                                         Query Match
Best Local Similarity 77.8%;
                                                     13
                                                                                                                                                             215 ĠPĹVĊNĠVĹ 223
                                                                                                                                         1 GPLVCRGTL 9
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                              165
                                                     18
                                                                                                                                                                                                                                                                                              KLK3 OR APS
                               VARSPLIC
                                                                          SEQUENCE
                                                     VARIANT
                                                                                                                                                                                                      K3_HUMAN
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SEQUENCE FROM N.A.

ISSUESHERS, and Prostate;

MEDLINE-22389257; PubMed=12477932;

MISUENE-22389257; PubMed=12477932;

RIAURHERST R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RAUGHORT R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A blachulo L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquilan R.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., Woffernan K.J., Maalek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahay J., Helton E., Woung A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length
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Riegman P.H.J., Vlietstra R.J., van der Korput J.A.G.M., Romijn J.C., Trapman J.;
"Characterization of the prostate-specific antigen gene: a novel human kallikrein-like gene.";
Biochem. Biophys. Res. Commun. 159:95-102(1989).
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MEDLINE=8808286; PubMed=3691515;
Schaller U., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.;
Schaller U, characterization and amino-acid sequence of gamma-seminoprotein, a glycoprotein from human seminal plasma.";
Eur. J. Biochem. 170:111-120(1987).
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Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19913 region.";
Gene 257:119-130(2000).
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Schulz P., Stucka R., Feldmann H., Combriato G., Klobeck H.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-261.
MEDLINE=86205857; PubMed=2422647;
Watt K.W.K., Lee P.J., M'Timkulu T., Chan W.P., Loor R.;
"Human prostate-specific antigen: structural and functional similarity will serine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 83:3166-3170(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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A -> T (IN REF. 11).
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                                                             Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
 64
                                                                                                                     215 GPLVCNGVL 223
                                                                                        1 GPLVCRGIL 9
                Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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ID KLK1 RAT
AC P00758;
 CONFLICT
                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                         coagulum.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-| Xaa.
-!- SIMILARITY: Belongs to peptidase family $1. Kallikrein subfamily.
 MEDLINE=95218633; PubMed=7535613;
Villoutreix B.O., Getzoff E.D., Griffin J.H.;
"A structural model for the prostate disease marker, human prostate-
                                                                                                   MEDLINE 984279960; PubMed = 9751643; Coombs G.S., Bergestrom R.C., Pellequer J.L., Baker S.I., Navre M., Smith M.M., Tainer J.A., Madison E.L., Corey D.R.; "Substrate specificity of prostate-specific antigen (PSA)."; Chem. Biol. 5:475-488 (1998).

-!- FUNCTION: Presumably hydrolyze the high molecular mass seminal vesicle protein thus leading to the liquefaction of the seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE.
PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0008236; F:serine-type peptidase activity; TAS.
Interpro; IPR009003; Cys. Ser. trypsin.
Interpro; IPR001254; Peptidase Si.
Interpro; IPR001314; Peptidase_SiA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S75755; AAD14185.1; ALT_INIT.
EMBL; M24543; AAA60193.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X07730; -; NOT ANNOTATED_CDS.
M27274; AAA60192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     CAB32124.1; ALT_SEQ.
CAB46487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                             Protein Sci. 3:2033-2044(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG33355.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C050595; AAH50595.2; -.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X14810; CAA32915.1; -. EMBL; X13940; CAA32123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               X13943; CAA32126.1; -.
X13944; CAA32127.1; -.
X05332; CAA28947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC005307; AAH05307.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; S01.162; -.
HGNC:6364; KLK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
65
120
213
69
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; AAA58802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1PFA; 26-JAN-95.
2PSA; 16-MAR-99.
                                                                                          3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A32297; A32297
                                                specific antigen.";
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213
213
69
31
50
1152
1152
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EMBL;
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EMBL;
EMBL;
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Wines D.R., Brady J.M., Pritochett D.B., Roberts J.L., Macdonald R.J.;
"Organization and expression of the rat kallikrein gene family.";
J. Biol. Chem. 264:7653-7662(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in kininogen to release Lys-bradykinin.
-!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in small molecule substrates. Highly selective action to release kalidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa or Leu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 48-261 FROM N.A.
MEDILIE=861131678; PubMed=3004582;
MEDILIE=861131678; PubMed=3004582;

"Immunological identification of rat tissue kallikrein CDNA and characterization of the kallikrein gene family.";

Biochim. Biophys. Acta 866:1-14 (1986).

-I- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=83117659; PubMed=6961406;
Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
"Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid
sequence of the encoded preproenzyme.";
Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
MEDLINE-89327211; PubMed=2753879;
Inoue H., Fukui K., Miyake Y.;
"Identification and structure of the rat true tissue kallikrein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Submaxillary gland;
MEDLINE=86051477; PubMed=2998455;
Ashley P.L., MacGonald R.J.;
AKAllkrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of four distinct types including tonin.";
Biochemistry 24:4512-4520(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 21, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
1-DEC-1998 (Rel. 37, Last annotation update)
Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue kallikrein) (PS kallikrein) (RGK-1).
                                                                            .
                                                                     2; Indels
80.0%; Score 40; DB 1; Length 261; 77.8%; Pred. No. 1.6; 2; Indels.ive 0; Mismatches 2; Indels.
                                                                                                                                                                                                                                                                                                                                                                                               261 AA.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 Primi, PRO0089; LTPS in Priming Priming Primi, Priming Primis Primis Primis Primis Primis Priming Primis Priming Primi
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MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9UKR0; Q9UKR1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Kallikrein 12 precursor (BC 3.4.21.-) (Kallikrein-like protein
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F2F99C0227A7882B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION PEPTIDE (PROBABLE).
GLANDULAR KALLIKREIN 1.
CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 261;
Pred. No. 2.5;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GYARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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                                                               EMBL; J00758; -; NOT ANNOTATED CDS.
EMBL; M11563; AAA41464.1; ALT_INIT.
EMBL; M23874; AAA41462.1; JOINED.
EMBL; M23875; AAA41462.1; JOINED.
EMBL; M23875; AAA41462.1; JOINED.
EMBL; D00446; BAA00346.1; JOINED.
EMBL; D00447; BAA00346.1; JOINED.
EMBL; X03560; CAAZ7247.1; -.
HSRP, A00944; KQRTP.
HSRP, P00757; 1SGF.
                                                                                                                                                                                                                                                                                 InterPro, IPR009003, Cys Ser trypsin.
InterPro, IPR001254, Peptidase_S1.
InterPro, IPR001314, Peptidase_S1A.
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Anticancer Res. 19:2843-2852(1999).
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28852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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RESOURCE FROM N.A. (ISGCOMNS 1 AND 2). Diamandis E.P.,

Yousef G.M. Madylara A. Socrilas A. Diamandis E.P.,

Yousef G.M. Madylara A. Socrilas A. Diamandis E.P.,

Toloning of new alternatively spliced forms of the Kallittein-like

RESOURCE FROM N.A. (ISGCOMN 1).

RESOURCE FROM N.A. (ISGCOMN 2).

RESOURCE FROM N.A. (ISGCOMN 3).

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Partial amino acid sequence of human factor D:homology with serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; IDIC; 22-JUL-99.
PDB; IFDP; 03-DBC-99.
PDB; IHFD; 22-JUN-99.
MEROPS; S01.191; -.
Genew; HGMC:2771; DF.
MIM; 134350; -.
                                                                    Davis A.E. III;
                                                                                                                                                                       resolution."
                                                                                                                                                                                                                                                                                                                                                                             missing
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PDB;
PDB;
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                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)
(Properdin factor D) (Adipsin).
    BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

KYVDWIRMIMENN -> NSTLVGLGTSWNFNSCQPF (in
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE OF 26-252.
MEDLINE-84108950; PubMed-6363133;
Obbison D.M.A., Gagnon J., Reid K.B.M.;
"Amino acid sequence of human factor D of the complement system.
Similarity in sequence between factor D and proteases of non-plasma
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 8-253 FROM N.A.
MEDLINE=92250520; PubMed=13/4388;
White R.T., Damm D., Hancock N., Rosen B.S., Lowell B.B., Usher P.,
White R.T., Spiegelman B.M.;
"Human adipsin is identical to complement factor D and is expressed
at high levels in adipose tissue.";
at high levels in adipose tissue.";
D. Biol. Chem. 267:9210-9213(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE OF 26-61 AND 194-220.
MEDLINE=64256515; PubMed=6821372;
MODINED D.M.A., Gagnon J., Reid K.B.M.;
"Pactor D of the alternative pathway of human complement.
Purification, alignment and N-terminal amino acid sequences of the major cyangen bromide fragments, and localization of the serine residue at the active site.;
Biochem. J. 187:863-874(1980).
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINESSO0441; PubMed=6383466; MEDLINESSO0441; PubMed=6383466; Memann M.A., Bhown A.S., Bennett J.C., Volanakis J.E.; "Amino acid sequence of human D of the alternative complement
                                                                                                               Match 16.0%; Score 38; DB 1; Length 248; Local Similarity 77.8%; Pred. No. 3.7; Onservative 0; Mismatches 2; Indels
                                                                     isoform 2).
/FTIG=VSP 005403.
MW; BB473E9@F8BAF703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=80145719; PubMed=6987665;
Volanakis J.E., Bhown A.S., Bennett J.C., Mole J.E.;
                                                                                                                                                                                                                                           253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flier J.S., Spiegelman B.M., Rosen B.M., Patent number WO9006365, 14-JUN-1990.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=6987665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 23:2482-2486(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   origin.";
FEBS Lett. 166:347-351(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE OF 26-82
                                                                                             26733
                                                                                                                                                                                                                                             STANDARD;
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222
222
248
248
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                                                                                               248 AA;
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                                                                                                                                                                1 GPLVCRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
       140
172
196
196
24
163
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       DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                SEQUENCE
                                                                                                                    Query Match
                                                                                                                                                                                                                                                       P00746;
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A Kim S., Narayana S.V., Volanakis J.E.;

"Crystal structure of a complement factor D mutant expressing
"Crystal structure of a complement factor D mutant expressing
"Crystal structure of a complement factor D with factor Chem. 270:4399-24405 [1950]

U Biol. Chem. 270:4399-24405 [1950]

U CAPLYTIC ACTIVITY: Cleaves factor B when the latter is complexed to that of Cls in the classical pathway. Its function is homologous to that of Cls in the classical pathway.

C -1 CAPLYTIC ACTIVITY: Cleaves component factor B (Arg. | -Lys) when in complex with C3b or with cobra venom factor (CVF).

C -1 SIMILARITY: Belongs to peptidase family $1.

Ref. 3 sequence had a peptide in the wrong order and another one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activity, TAS.

Activity, TAS.

By GO; GO:0008236; F:scrine-type peptidase activity; TAS.

CO; GO:0008236; F:scrine-type peptidase activity; TAS.

CO; GO:0008236; F:scrine-type peptidase activity; TAS.

CO; GO:0006508; P:proteolygis and peptidolygis; TAS.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

IN FRONTE; PR00125; CHYMOTRYPSIN.

IN FRNITS; PR00122; CHYMOTRYPSIN.

IN FROSITE; PS00134; TRYPSIN DOM; 1.

RROSITE; PS00135; TRYPSIN JD.

RROSITE; PROPED

RROSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94118317; PubMed=8289289; Natayana S.V.L., Carson M., Bl.Kabbani O., Kilpatrick J.M., Moore D., Narayana S.V.L., Carson M., Bl.Kabbani O., Kilpatrick J.M., Moore D., Chen X., Bugg C.F., Volanakis J.E., Delucas L.J.; Chen X., Bugg C.F., Volanakis J.E., Delucas L.J.; Structure of human factor D. A complement system protein at 2.0-A
                                                                                                                                                                                                                                                                                                                                                    "Active site amino acid sequence of human factor D.", Proc. Natl. Acad. Sci. U.S.A. 77:4938-4942(1980).
proteases.";
Proc. Natl. Acad. Sci. U.S.A. 77:1116-1119(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M84526; AAA35527.1; ALT_INIT.
                                                                                                                                                                   PARTIAL SEQUENCE OF 26-78,
MEDLINE=81054886; PubMed=6776531;
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1DFP, 25-FEB-98.
1DST, 11-UUL-96.
1DST, 17-AUG-96.
1DSO, 22-UUN-99.
1DIC, 22-UUL-99.
1FDP, 03-DEC-99.
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SEQUENCE OF 2-254 FROM N.A.

SEQUENCE OF 2-254; PubMed=9211743;

MEDLINE=97362044; PubMed=9211743;

Aveskogh M., Lutzelschwab C., Huang M.R., Hellman L.;

Aveskogh M., Lutzelschwab C., Huang M.R., Hellman L.;

("Meloblastine) and cathepsin G.";

Immunogenetics 46:181-191(1937)

- '- FUNCTION: Polymorphonuclear leukocyte serine protease that degrades elastin, fibronectin, laminin, vitronectin, and collagen types I, III, and IV (in vitro) and causes emphysema when administered by tracheal insufflation to hamsters (By similarity).

- '- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by preferential cleavage: Ala | -Xaa | -Xaa | -Xaa |

- '- SIMILARITY: Belongs to peptidase family SI. Elastase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99126347; PubMed=9925946; Sturrock A., Franklin K.F., Wu S.-Q., Hoidal J.R.; Carrock A., Franklin K.F., Wu S.-Q., Hoidal J.R.; Mouse proteinase-3 "Characterization and localization of the genes for mouse proteinase-3 (Prtn3) and neutrophil elastase (Elaz)."; Cytogenet. Cell Genet. 83:104-108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=129/Sv;
MEDLINE=9733029; PubMed=9187364;
Jenne D.E., Froehlich L., Hummel A.M., Specks U.;
"Cloning and functional expression of the murine homologue of proteinase 3: implications for the design of murine models of
                                                                                                                                                                                                                                     PRN3 MOUSE STANDARD; PRT; 254 AA.
61056; 008809;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myeloblastin precursor (BC 3.4.21.75) (Proteinase 3) (PR-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENOPS, SOL.134; -...
MED) MG1:89580; Prtn3.
MGD; MG1:89580; Prtn3.
InterPro; IPR001524; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
Pram; PR00189; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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                                                                                               210 ĠPĽVĆGĠVĽ 218
                                      1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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STRAIN=129/SvJ;
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                                                                                                                                                                                                                                                  1 -> M (IN REF. 1).

H -> F (IN REF. 6).

H -> V (IN REF. 6).

H -> E (IN REF. 4 AND 5).

G -> A (IN REF. 1 AND 2).

S -> T (IN REF. 1 AND 2).

S -> T (IN REF. 1 AND 2).

B -> G (IN REF. 4).

HSSING (IN REF. 4).

HSSING (IN REF. 4).

TCNRRTHHDGALTE -> KCRLYDVL (IN REF. 4).

MISSING (IN REF. 3).
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245
253 AA;
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-!- FUNCTION: Thrombin-like snake venom serine protease.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trimeresurus gramineus (Indian green tree viper) (Green habu snake). Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglosa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
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PROSITE, PS00134; TRYPSIN_HIS; 1.

Collagen degradation; Hydrolase; Serine protease; Signal; Zymogen; dignal.

Glagen degradation; Hydrolase; Serine protease; Signal; Zymogen; dignal.

1 27 BY SIMILARITY.

PROPEP 25 BY SIMILARITY.

CHAIN 30 250 MYELOBLASTIN.

ACT SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT SITE 205 CHARGE RELAY SYSTEM (BY SIMILARITY).

CARBOHYD 127 127 N'LINKED (GLCNAC. . ) (POTENTIAL).

CARBOHYD 176 176 N'LINKED (GLCNAC. . ) (POTENTIAL).
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Shimohigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Accelerated evolution of crotalinae snake venom gland serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 254; Pred. No. 3.8;
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S -> A (IN REF. 2).
W, 00CEB989A3CB79CA CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Venom serine proteinase 3 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009003; Cyg_Ser_trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1
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MEDLINE≈97096898; PubMed=8941719;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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013063;
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SP3_TRIGA
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060259; Q9HCB3; Q9UIL9; Q9UQ47;
15-UUL-1999 (Rel. 38, Last sequence update)
15-UAL-2099 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (MP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of tumor-associated differentially expressed gene-14, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hippocampus;
MEDLINE=88372070; PubMed=9714609;
Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
Sequence analysis and expression of human neuropsin cDNA and gene.";
Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.; novel form of human neuropsin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99413504; PubMed=10485494;
Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                        VENOM SERINE PROTEINASE 3.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. .) (POTENTIAL).
Score 38; DB 1; Length 258; Pred. No. 3.8;
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3160379F61E9F74B CRC64;
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                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 260:627-634(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99203457; Pubmed=10102990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIK8 OR PRSS19 OR TADG14 OR NRPN.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GPLICNGOL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 1
251 2
258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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General Processe Overcopressed by courism carcinoma.",

General Res. 58:4455-44591199)

General Res. 58:4455-44591199)

General Calibra R. Coron A.M. General Res. Wang K.;

General Res. 58:4455-4459190

Submitted (SERVIN)

Signification of a novel carrier control of a novel serior processe,

Signification of a novel carrier ```

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                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
A -> AACGSLDLLTKLYAENLPCVHLNPQWPSQPSHCPRG
WRSNPLPPAA (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=9363642; PubMed=7689340;
MEDLINE=9363642; PubMed=7689340;
Gauthier E.R., Chapdelaine P., Tremblay R.R., Dube J.Y.;
Gauthier E.R., Chapdelaine P., Tremblay R.R., Dube J.Y.;
Gauthier E.R., Chapdelaine P., Tremblay R.R., Dube J.Y.;
Biochim. Biophys. Acta 1174:207-210(1993).
I. PUNCTION: PSA presumably hydrolyzes the high molecular mass seminal vesicle protein thus leading to the liquefaction of the seminal coagulum. PSA is a glandular kallikrein.
I. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xa.
SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                 CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecines, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostate specific antigen precursor (EC 3.4.21.35) (FSA) (Gamma-seminoprotein) (Kallikrein 3).
KLK3 OR APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
SMART; SM00020; Tryp_SPc; 1.

PROSTTE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolaes; Serine protease; Glycoprotein; Zymogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                 76.0%; Score 38; DB 1; Length 260; 77.8%; Pred. No. 3.9; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                 EF439E5B8C83E660 CRC64;
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BY SIMILARITY.
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N-LINKED (GLCNAC.
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                                                                                                    POTENTIAL.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                    260 AA; 28048 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X73560; CAA51957.1; -. PIR; S35711; S35711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 GPLVCDGAL 222
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MEROPS; S01.162; -.
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                                                                                                    SIGNAL
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KLK3 MACMU
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
(Kallikrein 5 procesin 2) (KLK-L2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                    PROGYATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brattsand M., Egelrud T.;
"Purification, molecular cloning, and expression of a human stratum corneum trypsin-like serine protease with possible function in desquamation.";
J. Biol. Chem. 274:30033-30040(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINES-20118156. P. DubMed=10652563;

Yousef G.M., Luo L. Y., Diamandis E.P.;

"Identification of novel human kallikrein-like genes on chromosome".
                                                                                                                                   Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal.
SIGNAL 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJNE-20510030; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 3.9;
0; Mismatches 2; Indels
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                                                                                                                                                                       ACTIVATION PEPTIDE.
InterPro; IPR001254; Peptidase_S1.
InterPro; IRR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN HIS; I.
PROSITE; PS00134; TRYPSIN HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Stratum corneum;
MEDLINE=99445563; PubMed=10514489;
                                                                                                                                                                                                                                                                                                                                                                  28816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN REF. 3).
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(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R MIM; 605643; ...

R GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0005512; F:serine-type endopeptidase activity; NAS.

R GO; GO:000854; F:sepidermal differentiation; TAS.

R GO; GO:000854; F:sepidermal differentiation; TAS.

R GO; GO:0008508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR001314; Peptidase SI.

InterPro; IPR001314; Peptidase SI.

PRINTS; PR00172; CHYMOTRYPSIN.

DR PRINTS; PR00172; CHYMOTRYPSIN.

DR RNART; SN00129; TRYPSIN, I.

DR RNGSITE; PS50134; TRYPSIN, IIS; I.

RNGSITE; PS00134; TRYPSIN, IIS; I.

RNGSITE; PS00134; TRYPSIN, ERR; I.

RNGSITE; PS00134; TRYPSIN, ERR; I.

RHYDCLASE; Setine protease; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN REF. 3).
D92C92F5609E5946 CRC64;
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF168768, AAF03101.1; -.
EMBL, AF135028, AAD26429.1; -.
EMBL, AF243527, AAG33358.1; -.
EMBL, BC008036, AAH08036.1; -.
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231
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0 Query Match
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps

1 GPLVCRGTL 9 ||:|| |:| 247 GPVVCNGSL 255

arch completed: March 1, 2004, 17:30:00 b time: 7 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     March 1, 2004, 17:20:41; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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sp_virus:*
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# CUMMARIES

Query

Query

Match Length DB ID

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100.0 251 4 QBNFV7

90.0 251 11 Q9CQ78

82.0 249 11 Q9CQ78

82.0 249 11 Q9CQ78

82.0 612 2 QBNRX7

82.0 621 12 Q9R301

92.0 3201 2 Q9R321

93.0 3201 2 Q9R328

93.0 3201 2 Q9R30

94.0 3201 2 Q9R30

95.0 3201 2 Q9R30

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95.0 3201 2 Q9R30

96.0 354 6 Q9XSN6

90.0 257 13 Q8QG86

90.0 257 13 Q8QG86

90.0 257 13 Q8QG86

90.0 257 13 Q8QG86

90.0 257 14 Q8NCM4

90.0 257 15 Q8NCM5

90.0 257 16 Q9XRC9

90.0 257 17 Q8QG86

90.0 257 18 Q8CG86

90.0 257 19 Q8NCM5

90.0 257 19 Q8NCM5

90.0 257 10 Q8NCM5

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| aero<br>para<br>para<br>mus<br>mus<br>pomo<br>pomo<br>ratt<br>mus<br>mus<br>xant<br>mus<br>mus<br>mus<br>mus<br>mus<br>mus<br>mus<br>mus<br>mus<br>mus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Qechdo mus musculu<br>Q62540 mus spretus<br>Q9cvu2 mus musculu<br>Q9d974 mus musculu<br>Q9puf3 bothrops ja |
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| 0994BC2<br>099W7Q5<br>099W7Q5<br>099W7Q6<br>099CW76<br>099CW76<br>099UW33<br>099UW33<br>099UW33<br>099UW33<br>099UW33<br>099UW33<br>099UW33<br>099UW33<br>099UW34<br>099UW35<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW36<br>099UW3 | Q8CHD0<br>Q62540<br>Q9CVU2<br>Q9D974<br>Q9PUF3                                                             |
| 11441444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 11111                                                                                                      |
| 04100000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 1481<br>108<br>114<br>117                                                                                  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0.44<br>0.44<br>0.00<br>0.00                                                                               |
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| 11112121212121212121212121212121212121                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 4 4 4 4 4<br>4 6 6 4 8                                                                                     |

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RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last senotation update)
Kallikrein 7 (chymotryptic, stratum corneum).
Fuhmo sapiens (Human).
Fukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC032005; AAH32005.1;
GO; GO:0004263; F:chymctrypsin activity; IEA.
GO; GO:0008235; F:peptidase activity; IEA.
GO; GO:0006208; F:prypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase G1.
InterPro; IPR001314; Peptidase G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase, Protease, Serine protease.
SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DBQ8 PRELIMINARX; PRT; Q9DBQ8 (9DBQ8) (1-UN-2001 (TrEMBLrel. 17, Last seq. 01-CVT-2003 (TrEMBLrel. 17, Last seq. 01-CVT-2003 (TrEMBLrel. 25, Last anno. 1200016C12R1K protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan, PF00089, trypsin, 1.
PRINTS, PR00722, CHYMOTRYPSIN.
SMART, SM0020, Tryp SPC, 1.
PROSITE, PS50240, TRYPSIN DOM; 1.
PROSITE, PS00134, TRYPSIN HIS; 1.
PROSITE, PS00135, TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GPLVCRGTL 215
                                   135 GPLVCRGTL 143
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1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Best Local S
Matches 9
                                                                                                                                     Q8N5N9
Q8N5N9;
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29DBQ8
                                                                                                                      8N5N9
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Staki K., Okido T., Furunuo M., Aono H., Baldarella R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Gratinci S., Hill D., Hofmann M., Hume D.A., Kamiya M., Tee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sarok K., Sarok M., Sarok K., Sarok M., Sarok K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ryashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RH Hayashizaki Y., Runctional annotation of a full-length mouse cDNA collection."; RT Nature 409:685-690[200])

RE MBL, AKO04807; BARZ1579.1; -. SIMILARITY: BAZ23579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SIGNINGE FROM N.A.

STRAIN=CS7BL/6J; TISSUE=Tongue;

XX MEDLINE=21086660; PubMed=1121881;

XA ATAKAWA T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA AIZAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A AIZAWA T., IZAWA M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,

XA AIZAWA T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA AICAWA M., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml I.M., Staubli F., Suuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninfici P., Ge Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 1.1;
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MERCAS, SO1.307. -.

MGD, MGI.1921082; IE.200016G12Rik.

MGO, G0.0004233; Fichymotrypsin activity; IEA.

GO, G0.0004235; Firtypsin activity; IEA.

GO, G0.0004295; Firtypsin activity; IEA.

GO, G0.0004295; Firtypsin activity; IEA.

GO, G0.000529; Firtypsin activity; IEA.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR001214; Peptidase_S1.

InterPro; IPR001214; Peptidase_S1.

PRONITE; PR00722; CHYMOTRYPSIN.

SWART; SM00020; Tryp S60; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

RYGINGE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 25, Last annotation update)
2310015108Rik protein (Fragment).
PRSSZO OR 2310015108RK.
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88.9%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.97
...hag 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Ramioration of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hippostasin,
PMSSS20.
Mus musculus (Mouse).
Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
Mitsui S., Yamagushi N.;
Mitsui S., Yamagushi N.;
"CDNA cloning of a novel brain serine protease, Hippostasin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016226; BAA88825.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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TISSUBERAIN,
Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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F9FF9CB457D727D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          87 AA; 9549 MW; B988D0CD62926EAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              090TN4;
01-MXY-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 11;
Pred. No. 2.4;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 AA
                                                                                                    Nature 409:685-690(2001).

EMBL; AK0019102; BAB31548.1; --
HSSP; P00763; 1DP0.

MENOPS; 501.257; --
MGD; MG11929977; Prss20.

GO; GO:0005576; C:extracellular; IDA.

GO; GO:000576; C:extracellular; IDA.

InterPro; IPR0010254; Peptidage_S1.

Ffan; PF00089; trypsin; 1.

SWART; SW00000; TrypSsp; 1.

PROSITE; PS00135; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS, SO1.257; -.
MGD; MGI:1929977; Prss20.
GO; GO:005576; C:extracellular; IDA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00089; trypsin; 1.
PRINTS; PR07022; CTMVOTYPENIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               82.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.0
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GPLVCNGSL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPLVCRGTL 9
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SEQUENCE
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Length 249;

DB 11;

Score 41;

82.0%;

Query Match

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C STRAIN-C77BL/60; TISSUE=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiranka T., Hori F.,
Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojina Y., Konno H., Kodda M., Koya S., Kurihara C.,
A Rasuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tijma Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
The PANIN-CS7BL/6J; TISSUE-Tongue;
The PANIOM Consortium,
The PANIOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
HADALYSIS of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TERNELE1. 13, Last sequence update)
01-MAY-2000 (TERNELE1. 13, Last sequence update)
Hippostasin grostate type (Adult male tongue CDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full library, clone:2310040F07 product:protease, serine, asquence)
sequence).
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
VCBI_TaxID=10090;
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RIKEN FANTOM Consortium;

"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).
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                                   Indels
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Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Prostate;
MEDLINE=2052460; PubMed=11072088;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N
mitsui S., Okui A., Kominami E., Uemura H., Yamagushi N
mitsui S., Okui A., Kominami E.,
hichm cain/Tuse (PRS220) .";
Biochim. Biophys. Acta 1494:206-210(2000).
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MEDLINE=9279253; Pubmed=10349636;
Carninci P., Hayashizaki Y., Haya-fificiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                  276 AA
77.8%; Pred. No. 6.5; ive 1; Mismatches
   Local Similarity 77.8
nes 7; Conservative
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                                                                                                                                                                  204 GPLVCNGSL 212
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       Best Loc
Matches
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Q9QYN3
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Mol. Microbiol. 0:0-0(2003).
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Matches
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SEQUENCE FROM N.A.

STARIN-GSTBL/G61; TISSUE=Tongue;
STARIN-GSTBL/G61; TISSUE=Tongue;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
A Sumi N., Ishili Y.; Nakamura S., Hazama M., Nishine T., Harada A.,
A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
A Yoneda Y., Ishikawa Y., Ozawa K., Thora E., Matsuura S., Kawai J.,
A Yoneda Y., Ishikawa T., Ozawa K., Tinoue Y., Kira A., Hayashizaki Y.,
Chazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
T sequencing pipeline with 384 multicapillary sequencer.",
Genome Res. 10:1757-1771(2000).
                          SEQUENCE FROM N.A.
STRAIN=C57BL/G17 IISSUE=Tongue;
STRAIN=C57BL/G17 IISSUE=Tongue;
STRAIN=C57BL/G499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinashi H.; "The large linear plasmid pSLA2-L of Streptomyces rochei has an unusually condensed gene organization for secondary metabolism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 11; Length 276;
Pred. No. 7.2;
1; Mismatches 1; Indels
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    Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 GPLVCNGSL 239
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STRAIN=LOC 2705;

XM MEDINE=229497;

PERINE=LOC 2705;

PERINE=LOC 2705;

PERINE=LOC 2705;

PARAMETER C., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

Bessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

Pridmore R.D., Arigoni F.,

Pridmore R.D., Arigoni F.,

The genome sequence of Bifidobacterium longum reflects its adaptation of the human gastroinestinal tract.",

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

BENBL; AE014808; AAN25531.1;

CO; GO:0016849; F:ligase activity; IEA.

GO; GO:0016849; F:ligase activity; IEA.

GO; GO:0018152; P:metabolism; IEA.

GO; GO:0008152; P:metabolism; IEA.

RO; GO:0008152; P:metabolism; IEA.

RO; GO:0008153; AMP-bind.

DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; 1.

PROSITE; PS00687; ALDEHYDE DEHYDR GLU; 1.
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MEDLINE=2022173; PubMed=10767533;

Suwa M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H.,

Nimi O., Kinashi H.,

Nimit O., Kinashi H.,
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                                                                                                                                                          Hiratsu K., Mochizuki S., Kinashi H., "Cloning and analysis of the replication origin and the telomeres of the large linear plasmid pSLA2-L in Streptomyces rochei."; Mol. Gen. Genet. 263:1015-1021(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=7434AN4;
MEDINE=993344; PubMed=9836424;
MEDINE=9953144; PubMed=9836424;
Kinashi H., Shinkawa H.;
Kinashi H., Fujii S., Hatani A., Kurokawa T., Shinkawa H.;
Kinashi H., Fujii S., Hatani A., Kurokawa T., Shinkawa H.;
Fujii S., Hatani S., Hatani A., Furokawa T., Shinkawa H.;
Lhe eryal mapping of the linear plasmid psLA2-L and localization of the eryal and acti homologs ";
Biosci Biotechnol. Biochem. 62:1892-1897 (1998).
GO: 0046821; C:extrachromosomal DNA; IEA.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 25, Last annotation update)
Probable long-chain-fatty-acid--CoA ligase, long-chain acyl-CoA
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Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypotherical protein, Plasmid.
SEQUENCE 612 AA, 66525 MW, 9BF0E1EE8D3110FC CRC64,
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                                                                      STRAIN=7434AN4;
MEDLINE=20408175; PubMed=10954087;
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SEQUENCE FROM N.A.
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Q9F828

RESULT 9

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us-09-905-083-80.rspt

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 3546 AA, 371191 MW; 86C6794E95415BBC CRC64;
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01-0CT-2002 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
prostate specific antigen precursor.
                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 1.
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ENREL; AFAZESASA; AAG13917.1; -
HSSP; P25715; 1MLA.
GO; GO:0016491; F:roxidoreductase activity; IEA.
GO; GO:0016491; F:roxidoreductase activity; IEA.
GO; GO:0016631; F:transporter activity; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
GO; GO:0006125; F:transport; IEA.
GO; GO:000610; P:transport; IEA.
InterPro; IPR001299; ADH; Short.
InterPro; IPR001299; ADH; Short.
InterPro; IPR001299; ADH; Short.
InterPro; IPR006129; ADH; Short.
InterPro; IPR00613; Pp bind.
FEam; PF00109; RetCacyl-synt.; 2.
Ffam; PF00109; RetCacyl-synt.; 3.
FFAM; PF00109; RetCacyl-synt
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3546 AA.
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PRT;
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TISSUE=Prostate;
Heuze-Vourc'h N., Courty Y.;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NRRL3275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBNCW4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON CWA PRO CWA PAC COM CWA PAC           DDA TALLA TA
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora.
NCBI_TaxID=136926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; Score 41; DB 2; Length 3201; 77.8%; Pred. No. 77; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                    Query Match 82.0%; Score 41; DB 16; Length 621; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Phosphopantetheine; Transferase.
SEQUENCE 3201 AA; 334781 MW; 44BDA30E14855650 CRC64;
               Ligase; Complete proteome.
SEQUENCE 621 AA; 67948 MW; SBCDDB4B5BF3083A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEWBLrel. 16, Created)
11-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 3.
MEGAIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSOUGOS B KETOACKL SYNTHASE; 2. PROSITE; PSOUGL2; PHOSPHORANTETHEINE; 2. PROSITE; PSOUGS6: RCCT 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00698; Acyl_transf; 2.
Pfam; PF00106; adh short; 1.
Pfam; PF00109; Ketoacyl-synt, 2.
Pfam; PF02801; Ketoacyl-synt, C; 2.
Pfam; PF005801; Ketoacyl-synt, C; 2.
Pfam; PF00575; Thioseterase; 1.
PROSITE; PS50075; ACP_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SDR) FAMILY.
EMBL; AF263245; AAG13919.1; -.
HSSP; P25715; 1MLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.5
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1877 GPMVCRGGL 1885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 GPLVCRG 442
                                                                                                                                                                                                                                                                                                                                                              1 GPLVCRG 7
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Gaps

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RESULT 10 09F830

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The "Complex alternative splicing of the hKLK3 gene coding for the tumour warker PSA (prostate-specific-antigen).";

Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: BELONGS TO PEPTIDAGE FAMILY SI.

EMBL, AJ459782; CAD130844.1;

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004269; F:trypsin activity; IEA.

GO; GO:0006289; P:proteclysis activity; IEA.

InterPro; IPR001304; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

PROSTE: PS00202; CHYMOTRYBIN.

PROSITE; PS00202; CHYMOTRYBIN.

PROSITE; PS00135; TRYPSIN JIS; 1.

POTGRNIAL.

STORAL.

STORAL.

SEQUENCE 220 AA; 2431 MW; 15C8886A504A248D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEDLINE-98126310; PubMed=9465170;
Simmer J.P., Fukke M., Tanabe T., Yamakoshi Y., Uchida T., Xue J.,
Simmer J.P., Fukke M., DeHart B.C., Hu C.-C., Bartlett J.D.;
Margolis H.C., Shimizu M., DeHart B.C., Hu C.-C., Bartlett J.D.;
"Purification, characterization, and cloning of enamel matrix serine
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLINOV-1999 (TrEMBLrel. 12, Created)
OLINOV-1999 (TrEMBLrel. 12, Last sequence update)
OLIOCT-2003 (TrEMBLrel. 12, Last sequence update)
OLIOCT-2003 (TrEMBLrel. 25, Last annotation update)
Enamel matrix serine proteinase 1 precursor.
Enamel matrix serine proteinase 1 precursor.
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Protease, Serine protease, Signal.
24 POTENTIAL.
SIGNAL 1 24 POTENTIAL.
CHAIN 31 254 ENANEL MATEL.
SEQUENCE 254 AA, 27235 MW, FD40EF85664406F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 40; DB 4; Length 220; 77.8%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteinase 1.",
J. Dent. Res. 77:37-386(1998).
-!- SIMILARITY BELONGS TO PEPTIDASE FAMILY S1.
HSSP, P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.0
Tr. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 GPLVCNGVL 182
                                                                                                                                                                                                                                                                                                                                                                                                                            1 GPLVCRGTL 9
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Unqueira-de-Azevedo I.L.M., Ho P.L.;

Junqueira-de-Azevedo I.L.M., Ho P.L.;

Squence Tags (BSTS) ";

Squence Tags (BSTS) ";

Squence Tags (BSTS) ";

Squence Tags (BSTS) ";

Hasp; P00761; 1AN1.

CO; GO:0004263; Forbymotrypsin activity; IEA.

CO; GO:0004263; Fichymotrypsin activity; IEA.

CO; GO:0004263; Fichymotrypsin activity; IEA.

CO; GO:0004263; Fippidase activity; IEA.

CO; GO:0006508; Piproteolysis and peptidolysis; IEA.

CO; GO:0006508; Piproteolysis and peptidolysis; IEA.

InterPro; IPR001214; Peptidase S1.

InterPro; IPR001214; Peptidase S1.

InterPro; IPR001214; Peptidase S1.

InterPro; IPR00124; TRYPSIN.

RAMART; SM00200; TRYPSIN, 1.

PROSITE; PS00134; TRYPSIN HS; 1.

RAMART; SM00200; TRYPSIN HS; 1.

RAMART; SM00200; TRYPSIN HS; 1.

RAMART; SM00200; TRYPSIN HS; 1.

RAMART; SM0121; TRYPSIN HS; 1.

RAMART; SM0124; TRYPSIN HS; 1.

RAMART; SM0124; TRYPSIN HS; 1.

RAMART; SM0125; TRYPSIN JSR; 1.

RAMART; SM0126; TRYPSIN JSR; 1.
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEWBLrel. 21, Created)
01-JUN-2002 (TrEWBLrel. 21, Last sequence update)
01-JUN-2003 (TrEWBLrel. 25, Last annotation update)
Serine proteinase.
Bothrops insularis (Island jararaca) (Queimada jararaca).
Bothropta: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Streptomyces coelicolor.

Streptomycineae, Streptomycetaceae, Streptomyces.

MCB_TaxID=1902;
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Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels
Score 40; DB 6; Length 254; Pred. No. 10;
                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9XAC9,
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative aminoglycoside acetyltransferase.
SCO1927 OR SCC22.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 AA.
                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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     Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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209 GPLICNGSL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 GPLICNGT 212
                                                                                                                                                                                                                       1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPLVCRGT 8
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SEQUENCE FROM N.A.
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Q9XAC9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Praser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitech E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016991; F:gentamicin 3'-N-acetyltransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IPR003679; Antibiotic NAT. Plan; F:CS522; Antibiotic NAT. T. Transferase; Complete proteome: SEQUENCE 262 AA; 27930 MW; 0D239D41795A0B93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                             STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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TISSUB=Peripheral Nervous System;
Strauberg R.;
Submitted (PRR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050595; AAH50595.1;
GO; GO:0004263; F:chymetrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
   STRAIN=A3(2);
Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 3, (Prostate specific antigen) (Fragment)
Homo sapiens (Human).
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80.0%; Score 40; DB 16;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1;
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Nature 417:41-147(2002).
EMBL: AL939110; CAB50752.1; -.
PIR; T35999. T35999.
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SEQUENCE FROM N.A.
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DR InterPro; IPR001254; Peptidase_S1A.

DR PTAM: PP00089; LTypsin; 1.

DR PRINTS; PR00122; CHYMOTRYPSIN.

DR PRINTS; PR00122; CHYMOTRYPSIN.

DR PROSITE; PS00134; TRYPSIN, HIS; 1.

DR PROSITE; PS00134; TRYPSIN, HIS; 1.

DR PROSITE; PS00135; TRYPSIN, SER; 1.

FT NON TER.

Query Match

Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 1 GPLVCNGTL 9

DD 240 GPLVCNGVL 248

Search completed: March 1, 2004, 17:34:52
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